

SEQUENCE LISTING

<110> Baum, Peter R.
 Fanslow, William C.
 Lofton, Timothy E.
 Sorensen, Eric A.
 Youakim, Adel

<120> NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE THEREOF

<130> 3101-A

<140> Not yet assigned

<141> 2001-10-05

<150> 60/238,557

<151> 2000-10-05

<160> 39

<170> PatentIn version 3.1

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<223> nucleotides 1-21 are from Mus musculus Nectin-3, the rest are from human Nectin-3 alpha

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Gln Trp His Pro Ser Thr Ala Asp Ile Glu Asp Leu Ala Thr Glu Pro
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Asn Val Glu Asn Leu Asn Arg Phe Glu Arg Pro Met Asp Tyr Tyr Glu
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 355 360 365

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 370 375 380

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 385 390 395 400

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 Thr Ile Ala Thr Ile Ile Ala Ser Val Val Gly Gly Ala Leu Phe Ile
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gta ctt gta agt gtt ttg gct gga ata ttc tgc tat agg aga aga cgg 1296
 Val Leu Val Ser Val Leu Ala Gly Ile Phe Cys Tyr Arg Arg Arg Arg
 420 425 430

acg ttt cgt gga gac tac ttt gcc aag aac tac att cca cca tca gat 1344
 Thr Phe Arg Gly Asp Tyr Phe Ala Lys Asn Tyr Ile Pro Pro Ser Asp
 435 440 445

atg caa aaa gaa tca caa ata gat gtt ctt caa caa gat gag ctt gat 1392
 Met Gln Lys Glu Ser Gln Ile Asp Val Leu Gln Gln Asp Glu Leu Asp
 450 455 460

tct tac cca gac agt gta aaa aaa gaa aac aaa aat cca gtg aac aat 1440
 Ser Tyr Pro Asp Ser Val Lys Lys Glu Asn Lys Asn Pro Val Asn Asn
 465 470 475 480

cta ata cgt aaa gac tat tta gaa gag cct gaa aaa act cag tgg aac 1488
 Leu Ile Arg Lys Asp Tyr Leu Glu Glu Pro Glu Lys Thr Gln Trp Asn
 485 490 495

0927268-10504

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 Asn Val Glu Asn Leu Asn Arg Phe Glu Arg Pro Met Asp Tyr Tyr Glu
 500 505 510

gat cta aaa atg gga atg aag ttt gtc agt gat gaa cat tat gat gaa 1584
 Asp Leu Lys Met Gly Met Lys Phe Val Ser Asp Glu His Tyr Asp Glu
 515 520 525

aac gaa gat gac tta gtt tca cat gta gat ggt tcc gta att tcc agg 1632
 Asn Glu Asp Asp Leu Val Ser His Val Asp Gly Ser Val Ile Ser Arg
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 Arg Glu Trp Tyr Val
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Pro Pro Thr Pro Pro Pro Leu Leu Leu Leu Leu Phe Pro Leu Leu Leu
 35 40 45

Phe Ser Arg Leu Cys Gly Ala Leu Ala Gly Pro Ile Ile Val Glu Pro
 50 55 60

His Val Thr Ala Val Trp Gly Lys Asn Val Ser Leu Lys Cys Leu Ile
 65 70 75 80

Glu Val Asn Glu Thr Ile Thr Gln Ile Ser Trp Glu Lys Ile His Gly
 85 90 95

Lys Ser Ser Gln Thr Val Ala Val His His Pro Gln Tyr Gly Phe Ser
 100 105 110

Val Gln Gly Glu Tyr Gln Gly Arg Val Leu Phe Lys Asn Tyr Ser Leu
 115 120 125

Asn Asp Ala Thr Ile Thr Leu His Asn Ile Gly Phe Ser Asp Ser Gly
 130 135 140

Lys Tyr Ile Cys Lys Ala Val Thr Phe Pro Leu Gly Asn Ala Gln Ser
 145 150 155 160

Ser Thr Thr Val Thr Val Leu Val Glu Pro Thr Val Ser Leu Ile Lys
 165 170 175

Gly Pro Asp Ser Leu Ile Asp Gly Gly Asn Glu Thr Val Ala Ala Ile
 180 185 190

0907268-10501

Cys Ile Ala Ala Thr Gly Lys Pro Val Ala His Ile Asp Trp Glu Gly
 195 200 205
 Asp Leu Gly Glu Met Glu Ser Thr Thr Thr Ser Phe Pro Asn Glu Thr
 210 215 220
 Ala Thr Ile Ile Ser Gln Tyr Lys Leu Phe Pro Thr Arg Phe Ala Arg
 225 230 235 240
 Gly Arg Arg Ile Thr Cys Val Val Lys His Pro Ala Leu Glu Lys Asp
 245 250 255
 Ile Arg Tyr Ser Phe Ile Leu Asp Ile Gln Tyr Ala Pro Glu Val Ser
 260 265 270
 Val Thr Gly Tyr Asp Gly Asn Trp Phe Val Gly Arg Lys Gly Val Asn
 275 280 285
 Leu Lys Cys Asn Ala Asp Ala Asn Pro Pro Pro Phe Lys Ser Val Trp
 290 295 300
 Ser Arg Leu Asp Gly Gln Trp Pro Asp Gly Leu Leu Ala Ser Asp Asn
 305 310 315 320
 Thr Leu His Phe Val His Pro Leu Thr Phe Asn Tyr Ser Gly Val Tyr
 325 330 335
 Ile Cys Lys Val Thr Asn Ser Leu Gly Gln Arg Ser Asp Gln Lys Val
 340 345 350
 Ile Tyr Ile Ser Asp Pro Pro Thr Thr Thr Thr Leu Gln Pro Thr Ile
 355 360 365
 Gln Trp His Pro Ser Thr Ala Asp Ile Glu Asp Leu Ala Thr Glu Pro
 370 375 380
 Lys Lys Leu Pro Phe Pro Leu Ser Thr Leu Ala Thr Ile Lys Asp Asp
 385 390 395 400
 Thr Ile Ala Thr Ile Ile Ala Ser Val Val Gly Gly Ala Leu Phe Ile
 405 410 415
 Val Leu Val Ser Val Leu Ala Gly Ile Phe Cys Tyr Arg Arg Arg Arg
 420 425 430
 Thr Phe Arg Gly Asp Tyr Phe Ala Lys Asn Tyr Ile Pro Pro Ser Asp
 435 440 445
 Met Gln Lys Glu Ser Gln Ile Asp Val Leu Gln Gln Asp Glu Leu Asp
 450 455 460
 Ser Tyr Pro Asp Ser Val Lys Lys Glu Asn Lys Asn Pro Val Asn Asn
 465 470 475 480
 Leu Ile Arg Lys Asp Tyr Leu Glu Glu Pro Glu Lys Thr Gln Trp Asn
 485 490 495
 Asn Val Glu Asn Leu Asn Arg Phe Glu Arg Pro Met Asp Tyr Tyr Glu
 500 505 510

090722Z
 890201

Asp Leu Lys Met Gly Met Lys Phe Val Ser Asp Glu His Tyr Asp Glu
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Arg Glu Trp Tyr Val
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tct ctc ctc gga gcc ggg ctc ctg ctg cag ccc ccg acg cca cct ccg 96
Ser Leu Leu Gly Ala Gly Leu Leu Leu Gln Pro Pro Thr Pro Pro Pro
20 25 30
ctg ctg ctg ctg ctc ttc ccg ctg ctg ctc ttc tcc agg ctc tgt ggt 144
Leu Leu Leu Leu Leu Phe Pro Leu Leu Leu Phe Ser Arg Leu Cys Gly
35 40 45
gcc tta gct gga cca att att gtg gag cca cat gtc aca gca gta tgg 192
Ala Leu Ala Gly Pro Ile Ile Val Glu Pro His Val Thr Ala Val Trp
50 55 60
gga aag aat gtt tca tta aag tgt tta att gaa gta aat gaa acc ata 240
Gly Lys Asn Val Ser Leu Lys Cys Leu Ile Glu Val Asn Glu Thr Ile
65 70 75 80
aca cag att tca tgg gag aag ata cat ggc aaa agt tca cag act gtt 288
Thr Gln Ile Ser Trp Glu Lys Ile His Gly Lys Ser Ser Gln Thr Val
85 90 95
gca gtt cac cat ccc caa tat gga ttc tct gtt caa gga gaa tat cag 336
Ala Val His His Pro Gln Tyr Gly Phe Ser Val Gln Gly Glu Tyr Gln
100 105 110
gga aga gtc ttg ttt aaa aat tac tca ctt aat gat gca aca att act 384
Gly Arg Val Leu Phe Lys Asn Tyr Ser Leu Asn Asp Ala Thr Ile Thr
115 120 125
ctg cat aac ata gga ttc tct gat tct gga aaa tac atc tgc aaa gct 432
Leu His Asn Ile Gly Phe Ser Asp Ser Gly Lys Tyr Ile Cys Lys Ala
130 135 140
gtt aca ttc ccg ctt gga aat gcc cag tcc tct aca act gta act gtg 480
Val Thr Phe Pro Leu Gly Asn Ala Gln Ser Ser Thr Thr Val Thr Val
145 150 155 160

tta gtt gaa ccc act gtg agc ctg ata aaa ggg cca gat tct tta att 528
 Leu Val Glu Pro Thr Val Ser Leu Ile Lys Gly Pro Asp Ser Leu Ile
 165 170 175

gat gga gga aat gaa aca gta gca gcc att tgc atc gca gcc act gga 576
 Asp Gly Gly Asn Glu Thr Val Ala Ala Ile Cys Ile Ala Ala Thr Gly
 180 185 190

aaa ccc gtt gca cat att gac tgg gaa ggt gat ctt ggt gaa atg gaa 624
 Lys Pro Val Ala His Ile Asp Trp Glu Gly Asp Leu Gly Glu Met Glu
 195 200 205

tcc act aca act tct ttt cca aat gaa acg gca acg att atc agc cag 672
 Ser Thr Thr Thr Ser Phe Pro Asn Glu Thr Ala Thr Ile Ile Ser Gln
 210 215 220

tac aag cta ttt cca acc aga ttt gct aga gga agg cga att act tgt 720
 Tyr Lys Leu Phe Pro Thr Arg Phe Ala Arg Gly Arg Arg Ile Thr Cys
 225 230 235 240

gtt gta aaa cat cca gcc ttg gaa aag gac atc cga tac tct ttc ata 768
 Val Val Lys His Pro Ala Leu Glu Lys Asp Ile Arg Tyr Ser Phe Ile
 245 250 255

tta gac ata cag tat gct cct gaa gtt tcg gta aca gga tat gat gga 816
 Leu Asp Ile Gln Tyr Ala Pro Glu Val Ser Val Thr Gly Tyr Asp Gly
 260 265 270

aat tgg ttt gta gga aga aaa ggt gtt aat ctc aaa tgt aat gct gat 864
 Asn Trp Phe Val Gly Arg Lys Gly Val Asn Leu Lys Cys Asn Ala Asp
 275 280 285

gca aat cca cca ccc ttc aaa tct gtg tgg agc agg ttg gat gga caa 912
 Ala Asn Pro Pro Pro Phe Lys Ser Val Trp Ser Arg Leu Asp Gly Gln
 290 295 300

tgg cct gat ggt tta ttg gct tca gac aat act ctt cat ttt gtc cat 960
 Trp Pro Asp Gly Leu Leu Ala Ser Asp Asn Thr Leu His Phe Val His
 305 310 315 320

cca ttg act ttc aat tat tct ggt gtt tat atc tgt aaa gtg acc aat 1008
 Pro Leu Thr Phe Asn Tyr Ser Gly Val Tyr Ile Cys Lys Val Thr Asn
 325 330 335

tcc ctt ggt caa aga agt gac caa aaa gtc atc tac att tca gat gtt 1056
 Ser Leu Gly Gln Arg Ser Asp Gln Lys Val Ile Tyr Ile Ser Asp Val
 340 345 350

cca ttt aag cag acc tct tcc ata gct gta gct gga gcg gta att gga 1104
 Pro Phe Lys Gln Thr Ser Ser Ile Ala Val Ala Gly Ala Val Ile Gly
 355 360 365

gct gtt ctt gcc ctt ttc atc att gct atc ttt gtg act gtg ctg ctg 1152
 Ala Val Leu Ala Leu Phe Ile Ile Ala Ile Phe Val Thr Val Leu Leu
 370 375 380

act cct cga aaa aaa aga cca tcc tat ctt gac aaa gtg att gac ctt 1200
 Thr Pro Arg Lys Lys Arg Pro Ser Tyr Leu Asp Lys Val Ile Asp Leu
 385 390 395 400

0972263-100501

cca ccc aca cat aaa cca cct cct ctg tat gaa gaa cga tcc cca cct 1248
Pro Pro Thr His Lys Pro Pro Pro Leu Tyr Glu Glu Arg Ser Pro Pro
405 410 415

ttg cct cag aaa gac cta ttt cag cct gaa cac ttg cct ttg cag act 1296
Leu Pro Gln Lys Asp Leu Phe Gln Pro Glu His Leu Pro Leu Gln Thr
420 425 430

cag ttc aaa gaa aga gaa gtt ggc aat ctt cag cac tct aat gga cta 1344
Gln Phe Lys Glu Arg Glu Val Gly Asn Leu Gln His Ser Asn Gly Leu
435 440 445

aat agc agg agt ttt gac tat gaa gat gag aat cca gtt ggg gaa gat 1392
Asn Ser Arg Ser Phe Asp Tyr Glu Asp Glu Asn Pro Val Gly Glu Asp
450 455 460

ggc att cag cag atg tac ccc ctt tac aat caa atg tgc tac caa gac 1440
Gly Ile Gln Gln Met Tyr Pro Leu Tyr Asn Gln Met Cys Tyr Gln Asp
465 470 475 480

cgg agc cct ggc aaa cat cat caa aat aac gac cct aag aga gtc tac 1488
Arg Ser Pro Gly Lys His His Gln Asn Asn Asp Pro Lys Arg Val Tyr
485 490 495

atc gac cca cga gaa cat tat gtg tgatttttct cttttttccaa tgggcgttct 1542
Ile Asp Pro Arg Glu His Tyr Val
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aatagcaaat ttcttttctt cattaagcgt ttcttaacca ccagctgtgt ttgtgaactt 1722
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atttggattt ccctgacatg cttaatacaa ttacaatacc tgtgtacaaa cagaggcctg 2022
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 35 40 45
 Ala Leu Ala Gly Pro Ile Ile Val Glu Pro His Val Thr Ala Val Trp
 50 55 60
 Gly Lys Asn Val Ser Leu Lys Cys Leu Ile Glu Val Asn Glu Thr Ile
 65 70 75 80
 Thr Gln Ile Ser Trp Glu Lys Ile His Gly Lys Ser Ser Gln Thr Val
 85 90 95
 Ala Val His His Pro Gln Tyr Gly Phe Ser Val Gln Gly Glu Tyr Gln
 100 105 110
 Gly Arg Val Leu Phe Lys Asn Tyr Ser Leu Asn Asp Ala Thr Ile Thr
 115 120 125
 Leu His Asn Ile Gly Phe Ser Asp Ser Gly Lys Tyr Ile Cys Lys Ala
 130 135 140
 Val Thr Phe Pro Leu Gly Asn Ala Gln Ser Ser Thr Thr Val Thr Val
 145 150 155 160
 Leu Val Glu Pro Thr Val Ser Leu Ile Lys Gly Pro Asp Ser Leu Ile
 165 170 175
 Asp Gly Gly Asn Glu Thr Val Ala Ala Ile Cys Ile Ala Ala Thr Gly
 180 185 190
 Lys Pro Val Ala His Ile Asp Trp Glu Gly Asp Leu Gly Glu Met Glu
 195 200 205
 Ser Thr Thr Thr Ser Phe Pro Asn Glu Thr Ala Thr Ile Ile Ser Gln
 210 215 220
 Tyr Lys Leu Phe Pro Thr Arg Phe Ala Arg Gly Arg Arg Ile Thr Cys
 225 230 235 240
 Val Val Lys His Pro Ala Leu Glu Lys Asp Ile Arg Tyr Ser Phe Ile
 245 250 255
 Leu Asp Ile Gln Tyr Ala Pro Glu Val Ser Val Thr Gly Tyr Asp Gly
 260 265 270
 Asn Trp Phe Val Gly Arg Lys Gly Val Asn Leu Lys Cys Asn Ala Asp
 275 280 285
 Ala Asn Pro Pro Pro Phe Lys Ser Val Trp Ser Arg Leu Asp Gly Gln
 290 295 300
 Trp Pro Asp Gly Leu Leu Ala Ser Asp Asn Thr Leu His Phe Val His
 305 310 315 320
 Pro Leu Thr Phe Asn Tyr Ser Gly Val Tyr Ile Cys Lys Val Thr Asn
 325 330 335

0927268-10504

Ser Leu Gly Gln Arg Ser Asp Gln Lys Val Ile Tyr Ile Ser Asp Val
340 345 350

Pro Phe Lys Gln Thr Ser Ser Ile Ala Val Ala Gly Ala Val Ile Gly
355 360 365

Ala Val Leu Ala Leu Phe Ile Ile Ala Ile Phe Val Thr Val Leu Leu
370 375 380

Thr Pro Arg Lys Lys Arg Pro Ser Tyr Leu Asp Lys Val Ile Asp Leu
385 390 395 400

Pro Pro Thr His Lys Pro Pro Pro Leu Tyr Glu Glu Arg Ser Pro Pro
405 410 415

Leu Pro Gln Lys Asp Leu Phe Gln Pro Glu His Leu Pro Leu Gln Thr
420 425 430

Gln Phe Lys Glu Arg Glu Val Gly Asn Leu Gln His Ser Asn Gly Leu
435 440 445

Asn Ser Arg Ser Phe Asp Tyr Glu Asp Glu Asn Pro Val Gly Glu Asp
450 455 460

Gly Ile Gln Gln Met Tyr Pro Leu Tyr Asn Gln Met Cys Tyr Gln Asp
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Arg Ser Pro Gly Lys His His Gln Asn Asn Asp Pro Lys Arg Val Tyr
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Ile Asp Pro Arg Glu His Tyr Val
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from human Nectin-3 beta

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Ala Gln Leu Ser Ser Ala Ser Leu Leu Gly Ala Gly Leu Leu Leu Gln
20 25 30

ccc ccg acg cca cct ccg ctg ctg ctg ctg ctc ttc ccg ctg ctg ctc	144
Pro Pro Thr Pro Pro Pro Leu Leu Leu Leu Leu Phe Pro Leu Leu Leu	
35 40 45	
ttc tcc agg ctc tgt ggt gcc tta gct gga cca att att gtg gag cca	192
Phe Ser Arg Leu Cys Gly Ala Leu Ala Gly Pro Ile Ile Val Glu Pro	
50 55 60	
cat gtc aca gca gta tgg gga aag aat gtt tca tta aag tgt tta att	240
His Val Thr Ala Val Trp Gly Lys Asn Val Ser Leu Lys Cys Leu Ile	
65 70 75 80	
gaa gta aat gaa acc ata aca cag att tca tgg gag aag ata cat ggc	288
Glu Val Asn Glu Thr Ile Thr Gln Ile Ser Trp Glu Lys Ile His Gly	
85 90 95	
aaa agt tca cag act gtt gca gtt cac cat ccc caa tat gga ttc tct	336
Lys Ser Ser Gln Thr Val Ala Val His His Pro Gln Tyr Gly Phe Ser	
100 105 110	
gtt caa gga gaa tat cag gga aga gtc ttg ttt aaa aat tac tca ctt	384
Val Gln Gly Glu Tyr Gln Gly Arg Val Leu Phe Lys Asn Tyr Ser Leu	
115 120 125	
aat gat gca aca att act ctg cat aac ata gga ttc tct gat tct gga	432
Asn Asp Ala Thr Ile Thr Leu His Asn Ile Gly Phe Ser Asp Ser Gly	
130 135 140	
aaa tac atc tgc aaa gct gtt aca ttc ccg ctt gga aat gcc cag tcc	480
Lys Tyr Ile Cys Lys Ala Val Thr Phe Pro Leu Gly Asn Ala Gln Ser	
145 150 155 160	
tct aca act gta act gtg tta gtt gaa ccc act gtg agc ctg ata aaa	528
Ser Thr Thr Val Thr Val Leu Val Glu Pro Thr Val Ser Leu Ile Lys	
165 170 175	
ggg cca gat tct tta att gat gga gga aat gaa aca gta gca gcc att	576
Gly Pro Asp Ser Leu Ile Asp Gly Gly Asn Glu Thr Val Ala Ala Ile	
180 185 190	
tgc atc gca gcc act gga aaa ccc gtt gca cat att gac tgg gaa ggt	624
Cys Ile Ala Ala Thr Gly Lys Pro Val Ala His Ile Asp Trp Glu Gly	
195 200 205	
gat ctt ggt gaa atg gaa tcc act aca act tct ttt cca aat gaa acg	672
Asp Leu Gly Glu Met Glu Ser Thr Thr Thr Ser Phe Pro Asn Glu Thr	
210 215 220	
gca acg att atc agc cag tac aag cta ttt cca acc aga ttt gct aga	720
Ala Thr Ile Ile Ser Gln Tyr Lys Leu Phe Pro Thr Arg Phe Ala Arg	
225 230 235 240	
gga agg cga att act tgt gtt gta aaa cat cca gcc ttg gaa aag gac	768
Gly Arg Arg Ile Thr Cys Val Val Lys His Pro Ala Leu Glu Lys Asp	
245 250 255	
atc cga tac tct ttc ata tta gac ata cag tat gct cct gaa gtt tcg	816
Ile Arg Tyr Ser Phe Ile Leu Asp Ile Gln Tyr Ala Pro Glu Val Ser	
260 265 270	

0992260

gta aca gga tat gat gga aat tgg ttt gta gga aga aaa ggt gtt aat 864
Val Thr Gly Tyr Asp Gly Asn Trp Phe Val Gly Arg Lys Gly Val Asn
275 280 285

ctc aaa tgt aat gct gat gca aat cca cca ccc ttc aaa tct gtg tgg 912
Leu Lys Cys Asn Ala Asp Ala Asn Pro Pro Pro Phe Lys Ser Val Trp
290 295 300

agc agg ttg gat gga caa tgg cct gat ggt tta ttg gct tca gac aat 960
Ser Arg Leu Asp Gly Gln Trp Pro Asp Gly Leu Leu Ala Ser Asp Asn
305 310 315 320

act ctt cat ttt gtc cat cca ttg act ttc aat tat tct ggt gtt tat 1008
Thr Leu His Phe Val His Pro Leu Thr Phe Asn Tyr Ser Gly Val Tyr
325 330 335

atc tgt aaa gtg acc aat tcc ctt ggt caa aga agt gac caa aaa gtc 1056
Ile Cys Lys Val Thr Asn Ser Leu Gly Gln Arg Ser Asp Gln Lys Val
340 345 350

atc tac att tca gat gtt cca ttt aag cag acc tct tcc ata gct gta 1104
Ile Tyr Ile Ser Asp Val Pro Phe Lys Gln Thr Ser Ser Ile Ala Val
355 360 365

gct gga gcg gta att gga gct gtt ctt gcc ctt ttc atc att gct atc 1152
Ala Gly Ala Val Ile Gly Ala Val Leu Ala Leu Phe Ile Ile Ala Ile
370 375 380

ttt gtg act gtg ctg ctg act cct cga aaa aaa aga cca tcc tat ctt 1200
Phe Val Thr Val Leu Leu Thr Pro Arg Lys Lys Arg Pro Ser Tyr Leu
385 390 395 400

gac aaa gtg att gac ctt cca ccc aca cat aaa cca cct cct ctg tat 1248
Asp Lys Val Ile Asp Leu Pro Pro Thr His Lys Pro Pro Pro Leu Tyr
405 410 415

gaa gaa cga tcc cca cct ttg cct cag aaa gac cta ttt cag cct gaa 1296
Glu Glu Arg Ser Pro Pro Leu Pro Gln Lys Asp Leu Phe Gln Pro Glu
420 425 430

cac ttg cct ttg cag act cag ttc aaa gaa aga gaa gtt ggc aat ctt 1344
His Leu Pro Leu Gln Thr Gln Phe Lys Glu Arg Glu Val Gly Asn Leu
435 440 445

cag cac tct aat gga cta aat agc agg agt ttt gac tat gaa gat gag 1392
Gln His Ser Asn Gly Leu Asn Ser Arg Ser Phe Asp Tyr Glu Asp Glu
450 455 460

aat cca gtt ggg gaa gat ggc att cag cag atg tac ccc ctt tac aat 1440
Asn Pro Val Gly Glu Asp Gly Ile Gln Gln Met Tyr Pro Leu Tyr Asn
465 470 475 480

caa atg tgc tac caa gac cgg agc cct ggc aaa cat cat caa aat aac 1488
Gln Met Cys Tyr Gln Asp Arg Ser Pro Gly Lys His His Gln Asn Asn
485 490 495

gac cct aag aga gtc tac atc gac cca cga gaa cat tat gtg tga 1533
Asp Pro Lys Arg Val Tyr Ile Asp Pro Arg Glu His Tyr Val
500 505 510

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<210> 10
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<223> nucleotides 1-18 are from Mus musculus Nectin-3 DNA, the rest are from human Nectin-3 beta

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Ala Gln Leu Ser Ser Ala Ser Leu Leu Gly Ala Gly Leu Leu Leu Gln
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Pro Pro Thr Pro Pro Pro Leu Leu Leu Leu Leu Phe Pro Leu Leu Leu
 35 40 45

Phe Ser Arg Leu Cys Gly Ala Leu Ala Gly Pro Ile Ile Val Glu Pro
 50 55 60

His Val Thr Ala Val Trp Gly Lys Asn Val Ser Leu Lys Cys Leu Ile
 65 70 75 80

Glu Val Asn Glu Thr Ile Thr Gln Ile Ser Trp Glu Lys Ile His Gly
 85 90 95

Lys Ser Ser Gln Thr Val Ala Val His His Pro Gln Tyr Gly Phe Ser
 100 105 110

Val Gln Gly Glu Tyr Gln Gly Arg Val Leu Phe Lys Asn Tyr Ser Leu
 115 120 125

Asn Asp Ala Thr Ile Thr Leu His Asn Ile Gly Phe Ser Asp Ser Gly
 130 135 140

Lys Tyr Ile Cys Lys Ala Val Thr Phe Pro Leu Gly Asn Ala Gln Ser
 145 150 155 160

Ser Thr Thr Val Thr Val Leu Val Glu Pro Thr Val Ser Leu Ile Lys
 165 170 175

Gly Pro Asp Ser Leu Ile Asp Gly Gly Asn Glu Thr Val Ala Ala Ile
 180 185 190

Cys Ile Ala Ala Thr Gly Lys Pro Val Ala His Ile Asp Trp Glu Gly
 195 200 205

Asp Leu Gly Glu Met Glu Ser Thr Thr Thr Ser Phe Pro Asn Glu Thr
 210 215 220

Ala Thr Ile Ile Ser Gln Tyr Lys Leu Phe Pro Thr Arg Phe Ala Arg
 225 230 235 240

Gly Arg Arg Ile Thr Cys Val Val Lys His Pro Ala Leu Glu Lys Asp
 245 250 255

Ile Arg Tyr Ser Phe Ile Leu Asp Ile Gln Tyr Ala Pro Glu Val Ser
 260 265 270
 Val Thr Gly Tyr Asp Gly Asn Trp Phe Val Gly Arg Lys Gly Val Asn
 275 280 285
 Leu Lys Cys Asn Ala Asp Ala Asn Pro Pro Pro Phe Lys Ser Val Trp
 290 295 300
 Ser Arg Leu Asp Gly Gln Trp Pro Asp Gly Leu Leu Ala Ser Asp Asn
 305 310 315 320
 Thr Leu His Phe Val His Pro Leu Thr Phe Asn Tyr Ser Gly Val Tyr
 325 330 335
 Ile Cys Lys Val Thr Asn Ser Leu Gly Gln Arg Ser Asp Gln Lys Val
 340 345 350
 Ile Tyr Ile Ser Asp Val Pro Phe Lys Gln Thr Ser Ser Ile Ala Val
 355 360 365
 Ala Gly Ala Val Ile Gly Ala Val Leu Ala Leu Phe Ile Ile Ala Ile
 370 375 380
 Phe Val Thr Val Leu Leu Thr Pro Arg Lys Lys Arg Pro Ser Tyr Leu
 385 390 395 400
 Asp Lys Val Ile Asp Leu Pro Pro Thr His Lys Pro Pro Pro Leu Tyr
 405 410 415
 Glu Glu Arg Ser Pro Pro Leu Pro Gln Lys Asp Leu Phe Gln Pro Glu
 420 425 430
 His Leu Pro Leu Gln Thr Gln Phe Lys Glu Arg Glu Val Gly Asn Leu
 435 440 445
 Gln His Ser Asn Gly Leu Asn Ser Arg Ser Phe Asp Tyr Glu Asp Glu
 450 455 460
 Asn Pro Val Gly Glu Asp Gly Ile Gln Gln Met Tyr Pro Leu Tyr Asn
 465 470 475 480
 Gln Met Cys Tyr Gln Asp Arg Ser Pro Gly Lys His His Gln Asn Asn
 485 490 495
 Asp Pro Lys Arg Val Tyr Ile Asp Pro Arg Glu His Tyr Val
 500 505 510

<210> 11
 <211> 1533
 <212> DNA
 <213> homo sapiens

<220>
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<400> 11

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Met Ala Arg Thr Leu Arg Pro Ser Pro Leu Cys Pro Gly Gly Gly Lys	
1 5 10 15	
gca caa ctt tcc tcc gct tct ctc ctc gga gcc ggg ctc ctg ctg cag	96
Ala Gln Leu Ser Ser Ala Ser Leu Leu Gly Ala Gly Leu Leu Leu Gln	
20 25 30	
ccc ccg acg cca cct ccg ctg ctg ctg ctg ctc ttc ccg ctg ctg ctc	144
Pro Pro Thr Pro Pro Pro Leu Leu Leu Leu Leu Phe Pro Leu Leu Leu	
35 40 45	
ttc tcc agg ctc tgt ggt gcc tta gct gga cca att att gtg gag cca	192
Phe Ser Arg Leu Cys Gly Ala Leu Ala Gly Pro Ile Ile Val Glu Pro	
50 55 60	
cat gtc aca gca gta tgg gga aag aat gtt tca tta aag tgt tta att	240
His Val Thr Ala Val Trp Gly Lys Asn Val Ser Leu Lys Cys Leu Ile	
65 70 75 80	
gaa gta aat gaa acc ata aca cag att tca tgg gag aag ata cat ggc	288
Glu Val Asn Glu Thr Ile Thr Gln Ile Ser Trp Glu Lys Ile His Gly	
85 90 95	
aaa agt tca cag act gtt gca gtt cac cat ccc caa tat gga ttc tct	336
Lys Ser Ser Gln Thr Val Ala Val His His Pro Gln Tyr Gly Phe Ser	
100 105 110	
gtt caa gga gaa tat cag gga aga gtc ttg ttt aaa aat tac tca ctt	384
Val Gln Gly Glu Tyr Gln Gly Arg Val Leu Phe Lys Asn Tyr Ser Leu	
115 120 125	
aat gat gca aca att act ctg cat aac ata gga ttc tct gat tct gga	432
Asn Asp Ala Thr Ile Thr Leu His Asn Ile Gly Phe Ser Asp Ser Gly	
130 135 140	
aaa tac atc tgc aaa gct gtt aca ttc ccg ctt gga aat gcc cag tcc	480
Lys Tyr Ile Cys Lys Ala Val Thr Phe Pro Leu Gly Asn Ala Gln Ser	
145 150 155 160	
tct aca act gta act gtg tta gtt gaa ccc act gtg agc ctg ata aaa	528
Ser Thr Thr Val Thr Val Leu Val Glu Pro Thr Val Ser Leu Ile Lys	
165 170 175	
ggg cca gat tct tta att gat gga gga aat gaa aca gta gca gcc att	576
Gly Pro Asp Ser Leu Ile Asp Gly Gly Asn Glu Thr Val Ala Ala Ile	
180 185 190	
tgc atc gca gcc act gga aaa ccc gtt gca cat att gac tgg gaa ggt	624
Cys Ile Ala Ala Thr Gly Lys Pro Val Ala His Ile Asp Trp Glu Gly	
195 200 205	
gat ctt ggt gaa atg gaa tcc act aca act tct ttt cca aat gaa acg	672
Asp Leu Gly Glu Met Glu Ser Thr Thr Thr Ser Phe Pro Asn Glu Thr	
210 215 220	

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gca acg att atc agc cag tac aag cta ttt cca acc aga ttt gct aga 720
 Ala Thr Ile Ile Ser Gln Tyr Lys Leu Phe Pro Thr Arg Phe Ala Arg
 225 230 235 240

gga agg cga att act tgt gtt gta aaa cat cca gcc ttg gaa aag gac 768
 Gly Arg Arg Ile Thr Cys Val Val Lys His Pro Ala Leu Glu Lys Asp
 245 250 255

atc cga tac tct ttc ata tta gac ata cag tat gct cct gaa gtt tcg 816
 Ile Arg Tyr Ser Phe Ile Leu Asp Ile Gln Tyr Ala Pro Glu Val Ser
 260 265 270

gta aca gga tat gat gga aat tgg ttt gta gga aga aaa ggt gtt aat 864
 Val Thr Gly Tyr Asp Gly Asn Trp Phe Val Gly Arg Lys Gly Val Asn
 275 280 285

ctc aaa tgt aat gct gat gca aat cca cca ccc ttc aaa tct gtg tgg 912
 Leu Lys Cys Asn Ala Asp Ala Asn Pro Pro Pro Phe Lys Ser Val Trp
 290 295 300

agc agg ttg gat gga caa tgg cct gat ggt tta ttg gct tca gac aat 960
 Ser Arg Leu Asp Gly Gln Trp Pro Asp Gly Leu Leu Ala Ser Asp Asn
 305 310 315 320

act ctt cat ttt gtc cat cca ttg act ttc aat tat tct ggt gtt tat 1008
 Thr Leu His Phe Val His Pro Leu Thr Phe Asn Tyr Ser Gly Val Tyr
 325 330 335

atc tgt aaa gtg acc aat tcc ctt ggt caa aga agt gac caa aaa gtc 1056
 Ile Cys Lys Val Thr Asn Ser Leu Gly Gln Arg Ser Asp Gln Lys Val
 340 345 350

atc tac att tca gat gtt cca ttt aag cag acc tct tcc ata gct gta 1104
 Ile Tyr Ile Ser Asp Val Pro Phe Lys Gln Thr Ser Ser Ile Ala Val
 355 360 365

gct gga gcg gta att gga gct gtt ctt gcc ctt ttc atc att gct atc 1152
 Ala Gly Ala Val Ile Gly Ala Val Leu Ala Leu Phe Ile Ile Ala Ile
 370 375 380

ttt gtg act gtg ctg ctg act cct cga aaa aaa aga cca tcc tat ctt 1200
 Phe Val Thr Val Leu Leu Thr Pro Arg Lys Lys Arg Pro Ser Tyr Leu
 385 390 395 400

gac aaa gtg att gac ctt cca ccc aca cat aaa cca cct cct ctg tat 1248
 Asp Lys Val Ile Asp Leu Pro Pro Thr His Lys Pro Pro Pro Leu Tyr
 405 410 415

gaa gaa cga tcc cca cct ttg cct cag aaa gac cta ttt cag cct gaa 1296
 Glu Glu Arg Ser Pro Pro Leu Pro Gln Lys Asp Leu Phe Gln Pro Glu
 420 425 430

cac ttg cct ttg cag act cag ttc aaa gaa aga gaa gtt ggc aat ctt 1344
 His Leu Pro Leu Gln Thr Gln Phe Lys Glu Arg Glu Val Gly Asn Leu
 435 440 445

cag cac tct aat gga cta aat agc agg agt ttt gac tat gaa gat gag 1392
 Gln His Ser Asn Gly Leu Asn Ser Arg Ser Phe Asp Tyr Glu Asp Glu
 450 455 460

aat cca gtt ggg gaa gat ggc att cag cag atg tac ccc ctt tac aat 1440
 Asn Pro Val Gly Glu Asp Gly Ile Gln Gln Met Tyr Pro Leu Tyr Asn
 465 470 475 480

caa atg tgc tac caa gac cgg agc cct ggc aaa cat cat caa aat aac 1488
 Gln Met Cys Tyr Gln Asp Arg Ser Pro Gly Lys His His Gln Asn Asn
 485 490 495

gac cct aag aga gtc tac atc gac cca cga gaa cat tat gtg tga 1533
 Asp Pro Lys Arg Val Tyr Ile Asp Pro Arg Glu His Tyr Val
 500 505 510

<210> 12
 <211> 510
 <212> PRT
 <213> homo sapiens

<400> 12

Met Ala Arg Thr Leu Arg Pro Ser Pro Leu Cys Pro Gly Gly Gly Lys
 1 5 10 15

Ala Gln Leu Ser Ser Ala Ser Leu Leu Gly Ala Gly Leu Leu Leu Gln
 20 25 30

Pro Pro Thr Pro Pro Pro Leu Leu Leu Leu Leu Phe Pro Leu Leu Leu
 35 40 45

Phe Ser Arg Leu Cys Gly Ala Leu Ala Gly Pro Ile Ile Val Glu Pro
 50 55 60

His Val Thr Ala Val Trp Gly Lys Asn Val Ser Leu Lys Cys Leu Ile
 65 70 75 80

Glu Val Asn Glu Thr Ile Thr Gln Ile Ser Trp Glu Lys Ile His Gly
 85 90 95

Lys Ser Ser Gln Thr Val Ala Val His His Pro Gln Tyr Gly Phe Ser
 100 105 110

Val Gln Gly Glu Tyr Gln Gly Arg Val Leu Phe Lys Asn Tyr Ser Leu
 115 120 125

Asn Asp Ala Thr Ile Thr Leu His Asn Ile Gly Phe Ser Asp Ser Gly
 130 135 140

Lys Tyr Ile Cys Lys Ala Val Thr Phe Pro Leu Gly Asn Ala Gln Ser
 145 150 155 160

Ser Thr Thr Val Thr Val Leu Val Glu Pro Thr Val Ser Leu Ile Lys
 165 170 175

Gly Pro Asp Ser Leu Ile Asp Gly Gly Asn Glu Thr Val Ala Ala Ile
 180 185 190

Cys Ile Ala Ala Thr Gly Lys Pro Val Ala His Ile Asp Trp Glu Gly
 195 200 205

Asp Leu Gly Glu Met Glu Ser Thr Thr Thr Ser Phe Pro Asn Glu Thr
 210 215 220
 Ala Thr Ile Ile Ser Gln Tyr Lys Leu Phe Pro Thr Arg Phe Ala Arg
 225 230 235 240
 Gly Arg Arg Ile Thr Cys Val Val Lys His Pro Ala Leu Glu Lys Asp
 245 250 255
 Ile Arg Tyr Ser Phe Ile Leu Asp Ile Gln Tyr Ala Pro Glu Val Ser
 260 265 270
 Val Thr Gly Tyr Asp Gly Asn Trp Phe Val Gly Arg Lys Gly Val Asn
 275 280 285
 Leu Lys Cys Asn Ala Asp Ala Asn Pro Pro Pro Phe Lys Ser Val Trp
 290 295 300
 Ser Arg Leu Asp Gly Gln Trp Pro Asp Gly Leu Leu Ala Ser Asp Asn
 305 310 315 320
 Thr Leu His Phe Val His Pro Leu Thr Phe Asn Tyr Ser Gly Val Tyr
 325 330 335
 Ile Cys Lys Val Thr Asn Ser Leu Gly Gln Arg Ser Asp Gln Lys Val
 340 345 350
 Ile Tyr Ile Ser Asp Val Pro Phe Lys Gln Thr Ser Ser Ile Ala Val
 355 360 365
 Ala Gly Ala Val Ile Gly Ala Val Leu Ala Leu Phe Ile Ile Ala Ile
 370 375 380
 Phe Val Thr Val Leu Leu Thr Pro Arg Lys Lys Arg Pro Ser Tyr Leu
 385 390 395 400
 Asp Lys Val Ile Asp Leu Pro Pro Thr His Lys Pro Pro Pro Leu Tyr
 405 410 415
 Glu Glu Arg Ser Pro Pro Leu Pro Gln Lys Asp Leu Phe Gln Pro Glu
 420 425 430
 His Leu Pro Leu Gln Thr Gln Phe Lys Glu Arg Glu Val Gly Asn Leu
 435 440 445
 Gln His Ser Asn Gly Leu Asn Ser Arg Ser Phe Asp Tyr Glu Asp Glu
 450 455 460
 Asn Pro Val Gly Glu Asp Gly Ile Gln Gln Met Tyr Pro Leu Tyr Asn
 465 470 475 480
 Gln Met Cys Tyr Gln Asp Arg Ser Pro Gly Lys His His Gln Asn Asn
 485 490 495
 Asp Pro Lys Arg Val Tyr Ile Asp Pro Arg Glu His Tyr Val
 500 505 510

<210> 13
 <211> 634

<212> PRT

<213> Artificial Sequence

<220>

<223> fusion protein: human Nectin-3-alpha-Fc

<400> 13

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Met Ala Arg Thr Pro Gly Pro Ser Pro Leu Cys Pro Gly Gly Gly Lys
1          5          10          15

Ala Gln Leu Ser Ser Ala Ser Leu Leu Gly Ala Gly Leu Leu Leu Gln
          20          25          30

Pro Pro Thr Pro Pro Pro Leu Leu Leu Leu Leu Phe Pro Leu Leu Leu
          35          40          45

Phe Ser Arg Leu Cys Gly Ala Leu Ala Gly Pro Ile Ile Val Glu Pro
          50          55          60

His Val Thr Ala Val Trp Gly Lys Asn Val Ser Leu Lys Cys Leu Ile
65          70          75          80

Glu Val Asn Glu Thr Ile Thr Gln Ile Ser Trp Glu Lys Ile His Gly
          85          90          95

Lys Ser Ser Gln Thr Val Ala Val His His Pro Gln Tyr Gly Phe Ser
          100          105          110

Val Gln Gly Glu Tyr Gln Gly Arg Val Leu Phe Lys Asn Tyr Ser Leu
          115          120          125

Asn Asp Ala Thr Ile Thr Leu His Asn Ile Gly Phe Ser Asp Ser Gly
          130          135          140

Lys Tyr Ile Cys Lys Ala Val Thr Phe Pro Leu Gly Asn Ala Gln Ser
145          150          155          160

Ser Thr Thr Val Thr Val Leu Val Glu Pro Thr Val Ser Leu Ile Lys
          165          170          175

Gly Pro Asp Ser Leu Ile Asp Gly Gly Asn Glu Thr Val Ala Ala Ile
          180          185          190

Cys Ile Ala Ala Thr Gly Lys Pro Val Ala His Ile Asp Trp Glu Gly
          195          200          205

Asp Leu Gly Glu Met Glu Ser Thr Thr Thr Ser Phe Pro Asn Glu Thr
          210          215          220

Ala Thr Ile Ile Ser Gln Tyr Lys Leu Phe Pro Thr Arg Phe Ala Arg
225          230          235          240

Gly Arg Arg Ile Thr Cys Val Val Lys His Pro Ala Leu Glu Lys Asp
          245          250          255

Ile Arg Tyr Ser Phe Ile Leu Asp Ile Gln Tyr Ala Pro Glu Val Ser
          260          265          270

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Val Thr Gly Tyr Asp Gly Asn Trp Phe Val Gly Arg Lys Gly Val Asn
 275 280 285
 Leu Lys Cys Asn Ala Asp Ala Asn Pro Pro Pro Phe Lys Ser Val Trp
 290 295 300
 Ser Arg Leu Asp Gly Gln Trp Pro Asp Gly Leu Leu Ala Ser Asp Asn
 305 310 315 320
 Thr Leu His Phe Val His Pro Leu Thr Phe Asn Tyr Ser Gly Val Tyr
 325 330 335
 Ile Cys Lys Val Thr Asn Ser Leu Gly Gln Arg Ser Asp Gln Lys Val
 340 345 350
 Ile Tyr Ile Ser Asp Pro Pro Thr Thr Thr Thr Leu Gln Pro Thr Ile
 355 360 365
 Gln Trp His Pro Ser Thr Ala Asp Ile Glu Asp Leu Ala Thr Glu Pro
 370 375 380
 Lys Lys Leu Pro Phe Pro Leu Ser Thr Leu Ala Thr Ile Lys Asp Asp
 385 390 395 400
 Thr Ile Ala Thr Arg Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
 405 410 415
 Pro Ala Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro
 420 425 430
 Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
 435 440 445
 Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
 450 455 460
 Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
 465 470 475 480
 Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
 485 490 495
 His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
 500 505 510
 Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
 515 520 525
 Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
 530 535 540
 Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
 545 550 555 560
 Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
 565 570 575
 Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
 580 585 590

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Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
595 600 605

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
610 615 620

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
625 630

<210> 14

<211> 595

<212> PRT

<213> Artificial Sequence

<220>

<223> fusion protein: human Nectin-3-beta-Fc

<400> 14

Met Ala Arg Thr Pro Gly Pro Ser Pro Leu Cys Pro Gly Gly Gly Lys
1 5 10 15

Ala Gln Leu Ser Ser Ala Ser Leu Leu Gly Ala Gly Leu Leu Leu Gln
20 25 30

Pro Pro Thr Pro Pro Pro Leu Leu Leu Leu Leu Phe Pro Leu Leu Leu
35 40 45

Phe Ser Arg Leu Cys Gly Ala Leu Ala Gly Pro Ile Ile Val Glu Pro
50 55 60

His Val Thr Ala Val Trp Gly Lys Asn Val Ser Leu Lys Cys Leu Ile
65 70 75 80

Glu Val Asn Glu Thr Ile Thr Gln Ile Ser Trp Glu Lys Ile His Gly
85 90 95

Lys Ser Ser Gln Thr Val Ala Val His His Pro Gln Tyr Gly Phe Ser
100 105 110

Val Gln Gly Glu Tyr Gln Gly Arg Val Leu Phe Lys Asn Tyr Ser Leu
115 120 125

Asn Asp Ala Thr Ile Thr Leu His Asn Ile Gly Phe Ser Asp Ser Gly
130 135 140

Lys Tyr Ile Cys Lys Ala Val Thr Phe Pro Leu Gly Asn Ala Gln Ser
145 150 155 160

Ser Thr Thr Val Thr Val Leu Val Glu Pro Thr Val Ser Leu Ile Lys
165 170 175

Gly Pro Asp Ser Leu Ile Asp Gly Gly Asn Glu Thr Val Ala Ala Ile
180 185 190

Cys Ile Ala Ala Thr Gly Lys Pro Val Ala His Ile Asp Trp Glu Gly
195 200 205

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Asp Leu Gly Glu Met Glu Ser Thr Thr Thr Ser Phe Pro Asn Glu Thr
 210 215 220
 Ala Thr Ile Ile Ser Gln Tyr Lys Leu Phe Pro Thr Arg Phe Ala Arg
 225 230 235 240
 Gly Arg Arg Ile Thr Cys Val Val Lys His Pro Ala Leu Glu Lys Asp
 245 250 255
 Ile Arg Tyr Ser Phe Ile Leu Asp Ile Gln Tyr Ala Pro Glu Val Ser
 260 265 270
 Val Thr Gly Tyr Asp Gly Asn Trp Phe Val Gly Arg Lys Gly Val Asn
 275 280 285
 Leu Lys Cys Asn Ala Asp Ala Asn Pro Pro Pro Phe Lys Ser Val Trp
 290 295 300
 Ser Arg Leu Asp Gly Gln Trp Pro Asp Gly Leu Leu Ala Ser Asp Asn
 305 310 315 320
 Thr Leu His Phe Val His Pro Leu Thr Phe Asn Tyr Ser Gly Val Tyr
 325 330 335
 Ile Cys Lys Val Thr Asn Ser Leu Gly Gln Arg Ser Asp Gln Lys Val
 340 345 350
 Ile Tyr Ile Ser Asp Val Pro Phe Lys Gln Thr Ser Ser Arg Ser Cys
 355 360 365
 Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Glu Gly
 370 375 380
 Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
 385 390 395 400
 Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
 405 410 415
 Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
 420 425 430
 His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
 435 440 445
 Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
 450 455 460
 Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
 465 470 475 480
 Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
 485 490 495
 Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser
 500 505 510
 Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
 515 520 525

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
530 535 540

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
545 550 555 560

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
565 570 575

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
580 585 590

Pro Gly Lys
595

<210> 15
<211> 426
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion protein: human Nectin-3-alpha-FLAGpolyHis

<400> 15

Met Ala Arg Thr Pro Gly Pro Ser Pro Leu Cys Pro Gly Gly Gly Lys
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Ala Gln Leu Ser Ser Ala Ser Leu Leu Gly Ala Gly Leu Leu Leu Gln
20 25 30

Pro Pro Thr Pro Pro Pro Leu Leu Leu Leu Leu Phe Pro Leu Leu Leu
35 40 45

Phe Ser Arg Leu Cys Gly Ala Leu Ala Gly Pro Ile Ile Val Glu Pro
50 55 60

His Val Thr Ala Val Trp Gly Lys Asn Val Ser Leu Lys Cys Leu Ile
65 70 75 80

Glu Val Asn Glu Thr Ile Thr Gln Ile Ser Trp Glu Lys Ile His Gly
85 90 95

Lys Ser Ser Gln Thr Val Ala Val His His Pro Gln Tyr Gly Phe Ser
100 105 110

Val Gln Gly Glu Tyr Gln Gly Arg Val Leu Phe Lys Asn Tyr Ser Leu
115 120 125

Asn Asp Ala Thr Ile Thr Leu His Asn Ile Gly Phe Ser Asp Ser Gly
130 135 140

Lys Tyr Ile Cys Lys Ala Val Thr Phe Pro Leu Gly Asn Ala Gln Ser
145 150 155 160

Ser Thr Thr Val Thr Val Leu Val Glu Pro Thr Val Ser Leu Ile Lys
165 170 175

Gly Pro Asp Ser Leu Ile Asp Gly Gly Asn Glu Thr Val Ala Ala Ile
180 185 190

Cys Ile Ala Ala Thr Gly Lys Pro Val Ala His Ile Asp Trp Glu Gly
 195 200 205
 Asp Leu Gly Glu Met Glu Ser Thr Thr Thr Ser Phe Pro Asn Glu Thr
 210 215 220
 Ala Thr Ile Ile Ser Gln Tyr Lys Leu Phe Pro Thr Arg Phe Ala Arg
 225 230 235 240
 Gly Arg Arg Ile Thr Cys Val Val Lys His Pro Ala Leu Glu Lys Asp
 245 250 255
 Ile Arg Tyr Ser Phe Ile Leu Asp Ile Gln Tyr Ala Pro Glu Val Ser
 260 265 270
 Val Thr Gly Tyr Asp Gly Asn Trp Phe Val Gly Arg Lys Gly Val Asn
 275 280 285
 Leu Lys Cys Asn Ala Asp Ala Asn Pro Pro Pro Phe Lys Ser Val Trp
 290 295 300
 Ser Arg Leu Asp Gly Gln Trp Pro Asp Gly Leu Leu Ala Ser Asp Asn
 305 310 315 320
 Thr Leu His Phe Val His Pro Leu Thr Phe Asn Tyr Ser Gly Val Tyr
 325 330 335
 Ile Cys Lys Val Thr Asn Ser Leu Gly Gln Arg Ser Asp Gln Lys Val
 340 345 350
 Ile Tyr Ile Ser Asp Pro Pro Thr Thr Thr Thr Leu Gln Pro Thr Ile
 355 360 365
 Gln Trp His Pro Ser Thr Ala Asp Ile Glu Asp Leu Ala Thr Glu Pro
 370 375 380
 Lys Lys Leu Pro Phe Pro Leu Ser Thr Leu Ala Thr Ile Lys Asp Asp
 385 390 395 400
 Thr Ile Ala Thr Arg Ser Gly Ser Ser Asp Tyr Lys Asp Asp Asp Asp
 405 410 415
 Lys Gly Ser Ser His His His His His His
 420 425

<210> 16
 <211> 387
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> fusion protein: human Nectin-3-beta-FLAGpolyHis

<400> 16

Met Ala Arg Thr Pro Gly Pro Ser Pro Leu Cys Pro Gly Gly Gly Lys
 1 5 10 15

Ala Gln Leu Ser Ser Ala Ser Leu Leu Gly Ala Gly Leu Leu Leu Gln
 20 25 30
 Pro Pro Thr Pro Pro Pro Leu Leu Leu Leu Leu Phe Pro Leu Leu Leu
 35 40 45
 Phe Ser Arg Leu Cys Gly Ala Leu Ala Gly Pro Ile Ile Val Glu Pro
 50 55 60
 His Val Thr Ala Val Trp Gly Lys Asn Val Ser Leu Lys Cys Leu Ile
 65 70 75 80
 Glu Val Asn Glu Thr Ile Thr Gln Ile Ser Trp Glu Lys Ile His Gly
 85 90 95
 Lys Ser Ser Gln Thr Val Ala Val His His Pro Gln Tyr Gly Phe Ser
 100 105 110
 Val Gln Gly Glu Tyr Gln Gly Arg Val Leu Phe Lys Asn Tyr Ser Leu
 115 120 125
 Asn Asp Ala Thr Ile Thr Leu His Asn Ile Gly Phe Ser Asp Ser Gly
 130 135 140
 Lys Tyr Ile Cys Lys Ala Val Thr Phe Pro Leu Gly Asn Ala Gln Ser
 145 150 155 160
 Ser Thr Thr Val Thr Val Leu Val Glu Pro Thr Val Ser Leu Ile Lys
 165 170 175
 Gly Pro Asp Ser Leu Ile Asp Gly Gly Asn Glu Thr Val Ala Ala Ile
 180 185 190
 Cys Ile Ala Ala Thr Gly Lys Pro Val Ala His Ile Asp Trp Glu Gly
 195 200 205
 Asp Leu Gly Glu Met Glu Ser Thr Thr Thr Ser Phe Pro Asn Glu Thr
 210 215 220
 Ala Thr Ile Ile Ser Gln Tyr Lys Leu Phe Pro Thr Arg Phe Ala Arg
 225 230 235 240
 Gly Arg Arg Ile Thr Cys Val Val Lys His Pro Ala Leu Glu Lys Asp
 245 250 255
 Ile Arg Tyr Ser Phe Ile Leu Asp Ile Gln Tyr Ala Pro Glu Val Ser
 260 265 270
 Val Thr Gly Tyr Asp Gly Asn Trp Phe Val Gly Arg Lys Gly Val Asn
 275 280 285
 Leu Lys Cys Asn Ala Asp Ala Asn Pro Pro Pro Phe Lys Ser Val Trp
 290 295 300
 Ser Arg Leu Asp Gly Gln Trp Pro Asp Gly Leu Leu Ala Ser Asp Asn
 305 310 315 320
 Thr Leu His Phe Val His Pro Leu Thr Phe Asn Tyr Ser Gly Val Tyr
 325 330 335

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Ile Cys Lys Val Thr Asn Ser Leu Gly Gln Arg Ser Asp Gln Lys Val
340 345 350

Ile Tyr Ile Ser Asp Val Pro Phe Lys Gln Thr Ser Ser Arg Ser Gly
355 360 365

Ser Ser Asp Tyr Lys Asp Asp Asp Lys Gly Ser Ser His His His
370 375 380

His His His
385

<210> 17
<211> 549
<212> PRT
<213> mus musculus

<400> 17

Met Ala Arg Thr Pro Gly Pro Ala Pro Leu Cys Pro Gly Gly Gly Lys
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Ala Gln Leu Ser Ser Ala Phe Pro Pro Ala Ala Gly Leu Leu Leu Pro
20 25 30

Ala Pro Thr Pro Pro Pro Leu Leu Leu Leu Ile Pro Leu Leu Leu
35 40 45

Phe Ser Arg Leu Cys Gly Ala Leu Ala Gly Ser Ile Ile Val Glu Pro
50 55 60

His Val Thr Ala Val Trp Gly Lys Asn Val Ser Leu Lys Cys Leu Ile
65 70 75 80

Glu Val Asn Glu Thr Ile Thr Gln Ile Ser Trp Glu Lys Ile His Gly
85 90 95

Lys Ser Thr Gln Thr Val Ala Val His His Pro Gln Tyr Gly Phe Ser
100 105 110

Val Gln Gly Asp Tyr Gln Gly Arg Val Leu Phe Lys Asn Tyr Ser Leu
115 120 125

Asn Asp Ala Thr Ile Thr Leu His Asn Ile Gly Phe Ser Asp Ser Gly
130 135 140

Lys Tyr Ile Cys Lys Ala Val Thr Phe Pro Leu Gly Asn Ala Gln Ser
145 150 155 160

Ser Thr Thr Val Thr Val Leu Val Glu Pro Thr Val Ser Leu Ile Lys
165 170 175

Gly Pro Asp Ser Leu Ile Asp Gly Gly Asn Glu Thr Val Ala Ala Val
180 185 190

Cys Val Ala Ala Thr Gly Lys Pro Val Ala Gln Ile Asp Trp Glu Gly
195 200 205

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Asp Leu Gly Glu Met Glu Ser Ser Thr Thr Ser Phe Pro Asn Glu Thr
 210 215 220
 Ala Thr Ile Val Ser Gln Tyr Lys Leu Phe Pro Thr Arg Phe Ala Arg
 225 230 235 240
 Gly Arg Arg Ile Thr Cys Val Val Lys His Pro Ala Leu Glu Lys Asp
 245 250 255
 Ile Arg Tyr Ser Phe Ile Leu Asp Ile Gln Tyr Ala Pro Glu Val Ser
 260 265 270
 Val Thr Gly Tyr Asp Gly Asn Trp Phe Val Gly Arg Lys Gly Val Asn
 275 280 285
 Leu Lys Cys Asn Ala Asp Ala Asn Pro Pro Pro Phe Lys Ser Val Trp
 290 295 300
 Ser Arg Leu Asp Gly Gln Trp Pro Asp Gly Leu Leu Ala Ser Asp Asn
 305 310 315 320
 Thr Leu His Phe Val His Pro Leu Thr Val Asn Tyr Ser Gly Val Tyr
 325 330 335
 Val Cys Lys Val Ser Asn Ser Leu Gly Gln Arg Ser Asp Gln Lys Val
 340 345 350
 Ile Tyr Ile Ser Asp Pro Pro Thr Thr Thr Thr Leu Gln Pro Thr Val
 355 360 365
 Gln Trp His Ser Ser Pro Ala Asp Val Gln Asp Ile Ala Thr Glu His
 370 375 380
 Lys Lys Leu Pro Phe Pro Leu Ser Thr Leu Ala Thr Leu Lys Asp Asp
 385 390 395 400
 Thr Ile Gly Thr Ile Ile Ala Ser Val Val Gly Gly Ala Leu Phe Leu
 405 410 415
 Val Leu Val Ser Ile Leu Ala Gly Val Phe Cys Tyr Arg Arg Arg Arg
 420 425 430
 Thr Phe Arg Gly Asp Tyr Phe Ala Lys Asn Tyr Ile Pro Pro Ser Asp
 435 440 445
 Met Gln Lys Glu Ser Gln Ile Asp Val Leu His Gln Asp Glu Leu Asp
 450 455 460
 Ser Tyr Pro Asp Ser Val Lys Lys Glu Asn Lys Asn Pro Val Asn Asn
 465 470 475 480
 Leu Ile Arg Lys Asp Tyr Leu Glu Glu Pro Glu Lys Thr Gln Trp Asn
 485 490 495
 Asn Val Glu Asn Leu Thr Arg Phe Glu Arg Pro Met Asp Tyr Tyr Glu
 500 505 510
 Asp Leu Lys Met Gly Met Lys Phe Val Ser Asp Glu Arg Tyr Asn Glu
 515 520 525

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Ser Glu Asp Gly Leu Val Ser His Val Asp Gly Ser Val Ile Ser Arg
 530 535 540

Arg Glu Trp Tyr Val
 545

<210> 18
 <211> 510
 <212> PRT
 <213> mus musculus

<400> 18

Met Ala Arg Thr Pro Gly Pro Ala Pro Leu Cys Pro Gly Gly Gly Lys
 1 5 10 15

Ala Gln Leu Ser Ser Ala Phe Pro Pro Ala Ala Gly Leu Leu Leu Pro
 20 25 30

Ala Pro Thr Pro Pro Pro Leu Leu Leu Leu Leu Ile Pro Leu Leu Leu
 35 40 45

Phe Ser Arg Leu Cys Gly Ala Leu Ala Gly Ser Ile Ile Val Glu Pro
 50 55 60

His Val Thr Ala Val Trp Gly Lys Asn Val Ser Leu Lys Cys Leu Ile
 65 70 75 80

Glu Val Asn Glu Thr Ile Thr Gln Ile Ser Trp Glu Lys Ile His Gly
 85 90 95

Lys Ser Thr Gln Thr Val Ala Val His His Pro Gln Tyr Gly Phe Ser
 100 105 110

Val Gln Gly Asp Tyr Gln Gly Arg Val Leu Phe Lys Asn Tyr Ser Leu
 115 120 125

Asn Asp Ala Thr Ile Thr Leu His Asn Ile Gly Phe Ser Asp Ser Gly
 130 135 140

Lys Tyr Ile Cys Lys Ala Val Thr Phe Pro Leu Gly Asn Ala Gln Ser
 145 150 155 160

Ser Thr Thr Val Thr Val Leu Val Glu Pro Thr Val Ser Leu Ile Lys
 165 170 175

Gly Pro Asp Ser Leu Ile Asp Gly Gly Asn Glu Thr Val Ala Ala Val
 180 185 190

Cys Val Ala Ala Thr Gly Lys Pro Val Ala Gln Ile Asp Trp Glu Gly
 195 200 205

Asp Leu Gly Glu Met Glu Ser Ser Thr Thr Ser Phe Pro Asn Glu Thr
 210 215 220

Ala Thr Ile Val Ser Gln Tyr Lys Leu Phe Pro Thr Arg Phe Ala Arg
 225 230 235 240

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Gly Arg Arg Ile Thr Cys Val Val Lys His Pro Ala Leu Glu Lys Asp
 245 250 255
 Ile Arg Tyr Ser Phe Ile Leu Asp Ile Gln Tyr Ala Pro Glu Val Ser
 260 265 270
 Val Thr Gly Tyr Asp Gly Asn Trp Phe Val Gly Arg Lys Gly Val Asn
 275 280 285
 Leu Lys Cys Asn Ala Asp Ala Asn Pro Pro Pro Phe Lys Ser Val Trp
 290 295 300
 Ser Arg Leu Asp Gly Gln Trp Pro Asp Gly Leu Leu Ala Ser Asp Asn
 305 310 315 320
 Thr Leu His Phe Val His Pro Leu Thr Val Asn Tyr Ser Gly Val Tyr
 325 330 335
 Val Cys Lys Val Ser Asn Ser Leu Gly Gln Arg Ser Asp Gln Lys Val
 340 345 350
 Ile Tyr Ile Ser Asp Ile Pro Leu Thr Gln Thr Ser Ser Ile Ala Val
 355 360 365
 Ala Gly Ala Val Ile Gly Ala Val Leu Ala Leu Phe Ile Ile Thr Val
 370 375 380
 Phe Val Thr Val Leu Leu Thr Pro Arg Lys Lys Arg Pro Ser Tyr Leu
 385 390 395 400
 Asp Lys Val Ile Asp Leu Pro Pro Thr His Lys Pro Pro Pro Val Tyr
 405 410 415
 Glu Glu Arg Ile Pro Ser Leu Pro Gln Lys Asp Leu Leu Gly Gln Thr
 420 425 430
 Glu His Leu Pro Leu Gln Thr Gln Phe Lys Glu Lys Gly Ala Gly Gly
 435 440 445
 Leu Gln Pro Ser Asn Gly Pro Ile Ser Arg Arg Phe Asp Tyr Glu Asp
 450 455 460
 Glu Ser Thr Met Gln Glu Asp Gly Thr Gln Arg Met Cys Pro Leu Tyr
 465 470 475 480
 Ser Gln Met Cys His Gln Asp Arg Ser Pro Arg Gln His His Pro Arg
 485 490 495
 Asn Pro Glu Arg Leu Tyr Ile Asn Pro Arg Glu His Tyr Val
 500 505 510

<210> 19
 <211> 438
 <212> PRT
 <213> mus musculus
 <400> 19

39

Thr Leu His Phe Val His Pro Leu Thr Val Asn Tyr Ser Gly Val Tyr
325 330 335

Val Cys Lys Val Ser Asn Ser Leu Gly Gln Arg Ser Asp Gln Lys Val
340 345 350

Ile Tyr Ile Ser Asp Ile Pro Leu Thr Gln Thr Ser Ser Ile Ala Val
355 360 365

Ala Gly Ala Val Ile Gly Ala Val Leu Ala Leu Phe Ile Ile Thr Val
370 375 380

Phe Val Thr Val Leu Leu Thr Pro Arg Lys Lys Arg Pro Ser Tyr Leu
385 390 395 400

Asp Lys Val Ile Asp Leu Pro Pro Thr His Lys Pro Pro Pro Val Tyr
405 410 415

Glu Glu Arg Ile Pro Ser Leu Pro Gln Lys Asp Leu Leu Gly Gln Val
420 425 430

Arg Ala Leu Glu Asp Thr
435

<210> 20

<211> 517

<212> PRT

<213> homo sapiens

<400> 20

Met Ala Arg Met Gly Leu Ala Gly Ala Ala Gly Arg Trp Trp Gly Leu
1 5 10 15

Ala Leu Gly Leu Thr Ala Phe Phe Leu Pro Gly Val His Ser Gln Val
20 25 30

Val Gln Val Asn Asp Ser Met Tyr Gly Phe Ile Gly Thr Asp Val Val
35 40 45

Leu His Cys Ser Phe Ala Asn Pro Leu Pro Ser Val Lys Ile Thr Gln
50 55 60

Val Thr Trp Gln Lys Ser Thr Asn Gly Ser Lys Gln Asn Val Ala Ile
65 70 75 80

Tyr Asn Pro Ser Met Gly Val Ser Val Leu Ala Pro Tyr Arg Glu Arg
85 90 95

Val Glu Phe Leu Arg Pro Ser Phe Thr Asp Gly Thr Ile Arg Leu Ser
100 105 110

Arg Leu Glu Leu Glu Asp Glu Gly Val Tyr Ile Cys Glu Phe Ala Thr
115 120 125

Phe Pro Thr Gly Asn Arg Glu Ser Gln Leu Asn Leu Thr Val Met Ala
130 135 140

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Lys Pro Thr Asn Trp Ile Glu Gly Thr Gln Ala Val Leu Arg Ala Lys
 145 150 155 160
 Lys Gly Gln Asp Asp Lys Val Leu Val Ala Thr Cys Thr Ser Ala Asn
 165 170 175
 Gly Lys Pro Pro Ser Val Val Ser Trp Glu Thr Arg Leu Lys Gly Glu
 180 185 190
 Ala Glu Tyr Gln Glu Ile Arg Asn Pro Asn Gly Thr Val Thr Val Ile
 195 200 205
 Ser Arg Tyr Arg Leu Val Pro Ser Arg Glu Ala His Gln Gln Ser Leu
 210 215 220
 Ala Cys Ile Val Asn Tyr His Met Asp Arg Phe Lys Glu Ser Leu Thr
 225 230 235 240
 Leu Asn Val Gln Tyr Glu Pro Glu Val Thr Ile Glu Gly Phe Asp Gly
 245 250 255
 Asn Trp Tyr Leu Gln Arg Met Asp Val Lys Leu Thr Cys Lys Ala Asp
 260 265 270
 Ala Asn Pro Pro Ala Thr Glu Tyr His Trp Thr Thr Leu Asn Gly Ser
 275 280 285
 Leu Pro Lys Gly Val Glu Ala Gln Asn Arg Thr Leu Phe Phe Lys Gly
 290 295 300
 Pro Ile Asn Tyr Ser Leu Ala Gly Thr Tyr Ile Cys Glu Ala Thr Asn
 305 310 315 320
 Pro Ile Gly Thr Arg Ser Gly Gln Val Glu Val Asn Ile Thr Glu Phe
 325 330 335
 Pro Tyr Thr Pro Ser Pro Pro Glu His Gly Arg Arg Ala Gly Pro Val
 340 345 350
 Pro Thr Ala Ile Ile Gly Gly Val Ala Gly Ser Ile Leu Leu Val Leu
 355 360 365
 Ile Val Val Gly Gly Ile Val Val Ala Leu Arg Arg Arg Arg His Thr
 370 375 380
 Phe Lys Gly Asp Tyr Ser Thr Lys Lys His Val Tyr Gly Asn Gly Tyr
 385 390 395 400
 Ser Lys Ala Gly Ile Pro Gln His His Pro Pro Met Ala Gln Asn Leu
 405 410 415
 Gln Tyr Pro Asp Asp Ser Asp Asp Glu Lys Lys Ala Gly Pro Leu Gly
 420 425 430
 Gly Ser Ser Tyr Glu Glu Glu Glu Glu Glu Glu Gly Gly Gly Gly
 435 440 445
 Gly Glu Arg Lys Val Gly Gly Pro His Pro Lys Tyr Asp Glu Asp Ala
 450 455 460

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Lys Arg Pro Tyr Phe Thr Val Asp Glu Ala Glu Ala Arg Gln Asp Gly
465 470 475 480

Tyr Gly Asp Arg Thr Leu Gly Tyr Gln Tyr Asp Pro Glu Gln Leu Asp
485 490 495

Leu Ala Glu Asn Met Val Ser Gln Asn Asp Gly Ser Phe Ile Ser Lys
500 505 510

Lys Glu Trp Tyr Val
515

<210> 21
<211> 458
<212> PRT
<213> homo sapiens

<400> 21

Met Ala Arg Met Gly Leu Ala Gly Ala Ala Gly Arg Trp Trp Gly Leu
1 5 10 15

Ala Leu Gly Leu Thr Ala Phe Phe Leu Pro Gly Val His Ser Gln Val
20 25 30

Val Gln Val Asn Asp Ser Met Tyr Gly Phe Ile Gly Thr Asp Val Val
35 40 45

Leu His Cys Ser Phe Ala Asn Pro Leu Pro Ser Val Lys Ile Thr Gln
50 55 60

Val Thr Trp Gln Lys Ser Thr Asn Gly Ser Lys Gln Asn Val Ala Ile
65 70 75 80

Tyr Asn Pro Ser Met Gly Val Ser Val Leu Ala Pro Tyr Arg Glu Arg
85 90 95

Val Glu Phe Leu Arg Pro Ser Phe Thr Asp Gly Thr Ile Arg Leu Ser
100 105 110

Arg Leu Glu Leu Glu Asp Glu Gly Val Tyr Ile Cys Glu Phe Ala Thr
115 120 125

Phe Pro Thr Gly Asn Arg Glu Ser Gln Leu Asn Leu Thr Val Met Ala
130 135 140

Lys Pro Thr Asn Trp Ile Glu Gly Thr Gln Ala Val Leu Arg Ala Lys
145 150 155 160

Lys Gly Gln Asp Asp Lys Val Leu Val Ala Thr Cys Thr Ser Ala Asn
165 170 175

Gly Lys Pro Pro Ser Val Val Ser Trp Glu Thr Arg Leu Lys Gly Glu
180 185 190

Ala Glu Tyr Gln Glu Ile Arg Asn Pro Asn Gly Thr Val Thr Val Ile
195 200 205

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Ser Arg Tyr Arg Leu Val Pro Ser Arg Glu Ala His Gln Gln Ser Leu
210 215 220

Ala Cys Ile Val Asn Tyr His Met Asp Arg Phe Lys Glu Ser Leu Thr
225 230 235 240

Leu Asn Val Gln Tyr Glu Pro Glu Val Thr Ile Glu Gly Phe Asp Gly
245 250 255

Asn Trp Tyr Leu Gln Arg Met Asp Val Lys Leu Thr Cys Lys Ala Asp
260 265 270

Ala Asn Pro Pro Ala Thr Glu Tyr His Trp Thr Thr Leu Asn Gly Ser
275 280 285

Leu Pro Lys Gly Val Glu Ala Gln Asn Arg Thr Leu Phe Phe Lys Gly
290 295 300

Pro Ile Asn Tyr Ser Leu Ala Gly Thr Tyr Ile Cys Glu Ala Thr Asn
305 310 315 320

Pro Ile Gly Thr Arg Ser Gly Gln Val Glu Val Asn Ile Thr Glu Lys
325 330 335

Pro Arg Pro Gln Arg Gly Leu Gly Ser Ala Ala Arg Leu Leu Ala Gly
340 345 350

Thr Val Ala Val Phe Leu Ile Leu Val Ala Val Leu Thr Val Phe Phe
355 360 365

Leu Tyr Asn Arg Gln Gln Lys Ser Pro Pro Glu Thr Asp Gly Ala Gly
370 375 380

Thr Asp Gln Pro Leu Ser Gln Lys Pro Glu Pro Ser Pro Ser Arg Gln
385 390 395 400

Ser Ser Leu Val Pro Glu Asp Ile Gln Val Val His Leu Asp Pro Gly
405 410 415

Arg Gln Gln Gln Gln Glu Glu Glu Asp Leu Gln Lys Leu Ser Leu Gln
420 425 430

Pro Pro Tyr Tyr Asp Leu Gly Val Ser Pro Ser Tyr His Pro Ser Val
435 440 445

Arg Thr Thr Glu Pro Arg Gly Glu Cys Pro
450 455

<210> 22

<211> 479

<212> PRT

<213> homo sapiens

<400> 22

Met Ala Arg Ala Ala Ala Leu Leu Pro Ser Arg Ser Pro Pro Thr Pro
1 5 10 15

Leu Leu Trp Pro Leu Leu Leu Leu Leu Leu Leu Glu Thr Gly Ala Gln
20 25 30

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Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly Gly
 35 40 45
 Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu Tyr
 50 55 60
 Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His Gln
 65 70 75 80
 Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser Pro
 85 90 95
 Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser Thr
 100 105 110
 Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu His
 115 120 125
 Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Ala Thr
 130 135 140
 Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu Arg Val Ile Ala
 145 150 155 160
 Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln Asp
 165 170 175
 Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro Ala
 180 185 190
 Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr Gln
 195 200 205
 Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe Thr
 210 215 220
 Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys Val
 225 230 235 240
 Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu Ser
 245 250 255
 Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn Trp
 260 265 270
 Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser Asn
 275 280 285
 Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe Pro
 290 295 300
 Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val Asp
 305 310 315 320
 Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val Gly
 325 330 335

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 093268-100501

Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Arg Ala
340 345 350

Ser Pro Arg Asp Val Gly Pro Leu Val Trp Gly Ala Val Gly Gly Thr
355 360 365

Leu Leu Val Leu Leu Leu Leu Ala Gly Gly Ser Leu Ala Phe Ile Leu
370 375 380

Leu Arg Val Arg Arg Arg Arg Lys Ser Pro Gly Gly Ala Gly Gly Gly
385 390 395 400

Ala Ser Gly Asp Gly Gly Phe Tyr Asp Pro Lys Ala Gln Val Leu Gly
405 410 415

Asn Gly Asp Pro Val Phe Trp Thr Pro Val Val Pro Gly Pro Met Glu
420 425 430

Pro Asp Gly Lys Asp Glu Glu Glu Glu Glu Glu Glu Lys Ala Glu
435 440 445

Lys Gly Leu Met Leu Pro Pro Pro Pro Ala Leu Glu Asp Asp Met Glu
450 455 460

Ser Gln Leu Asp Gly Ser Leu Ile Ser Arg Arg Ala Val Tyr Val
465 470 475

<210> 23

<211> 538

<212> PRT

<213> homo sapiens

<400> 23

Met Ala Arg Ala Ala Ala Leu Leu Pro Ser Arg Ser Pro Pro Thr Pro
1 5 10 15

Leu Leu Trp Pro Leu Leu Leu Leu Leu Leu Leu Glu Thr Gly Ala Gln
20 25 30

Asp Val Arg Val Gln Val Leu Pro Glu Val Arg Gly Gln Leu Gly Gly
35 40 45

Thr Val Glu Leu Pro Cys His Leu Leu Pro Pro Val Pro Gly Leu Tyr
50 55 60

Ile Ser Leu Val Thr Trp Gln Arg Pro Asp Ala Pro Ala Asn His Gln
65 70 75 80

Asn Val Ala Ala Phe His Pro Lys Met Gly Pro Ser Phe Pro Ser Pro
85 90 95

Lys Pro Gly Ser Glu Arg Leu Ser Phe Val Ser Ala Lys Gln Ser Thr
100 105 110

Gly Gln Asp Thr Glu Ala Glu Leu Gln Asp Ala Thr Leu Ala Leu His
115 120 125

Gly Leu Thr Val Glu Asp Glu Gly Asn Tyr Thr Cys Glu Phe Ala Thr
130 135 140

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Phe Pro Lys Gly Ser Val Arg Gly Met Thr Trp Leu Arg Val Ile Ala
 145 150 155 160
 Lys Pro Lys Asn Gln Ala Glu Ala Gln Lys Val Thr Phe Ser Gln Asp
 165 170 175
 Pro Thr Thr Val Ala Leu Cys Ile Ser Lys Glu Gly Arg Pro Pro Ala
 180 185 190
 Arg Ile Ser Trp Leu Ser Ser Leu Asp Trp Glu Ala Lys Glu Thr Gln
 195 200 205
 Val Ser Gly Thr Leu Ala Gly Thr Val Thr Val Thr Ser Arg Phe Thr
 210 215 220
 Leu Val Pro Ser Gly Arg Ala Asp Gly Val Thr Val Thr Cys Lys Val
 225 230 235 240
 Glu His Glu Ser Phe Glu Glu Pro Ala Leu Ile Pro Val Thr Leu Ser
 245 250 255
 Val Arg Tyr Pro Pro Glu Val Ser Ile Ser Gly Tyr Asp Asp Asn Trp
 260 265 270
 Tyr Leu Gly Arg Thr Asp Ala Thr Leu Ser Cys Asp Val Arg Ser Asn
 275 280 285
 Pro Glu Pro Thr Gly Tyr Asp Trp Ser Thr Thr Ser Gly Thr Phe Pro
 290 295 300
 Thr Ser Ala Val Ala Gln Gly Ser Gln Leu Val Ile His Ala Val Asp
 305 310 315 320
 Ser Leu Phe Asn Thr Thr Phe Val Cys Thr Val Thr Asn Ala Val Gly
 325 330 335
 Met Gly Arg Ala Glu Gln Val Ile Phe Val Arg Glu Thr Pro Asn Thr
 340 345 350
 Ala Gly Ala Gly Ala Thr Gly Gly Ile Ile Gly Gly Ile Ile Ala Ala
 355 360 365
 Ile Ile Ala Thr Ala Val Ala Ala Thr Gly Ile Leu Ile Cys Arg Gln
 370 375 380
 Gln Arg Lys Glu Gln Thr Leu Gln Gly Ala Glu Glu Asp Glu Asp Leu
 385 390 395 400
 Glu Gly Pro Pro Ser Tyr Lys Pro Pro Thr Pro Lys Ala Lys Leu Glu
 405 410 415
 Ala Gln Glu Met Pro Ser Gln Leu Phe Thr Leu Gly Ala Ser Glu His
 420 425 430
 Ser Pro Leu Lys Thr Pro Tyr Phe Asp Ala Gly Ala Ser Cys Thr Glu
 435 440 445
 Gln Glu Met Pro Arg Tyr His Glu Leu Pro Thr Leu Glu Glu Arg Ser
 450 455 460

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Gly Pro Leu His Pro Gly Ala Thr Ser Leu Gly Ser Pro Ile Pro Val
 465 470 475 480

Pro Pro Gly Pro Pro Ala Val Glu Asp Val Ser Leu Asp Leu Glu Asp
 485 490 495

Glu Glu Gly Glu Glu Glu Glu Glu Tyr Leu Asp Lys Ile Asn Pro Ile
 500 505 510

Tyr Asp Ala Leu Ser Tyr Ser Ser Pro Ser Asp Ser Tyr Gln Gly Lys
 515 520 525

Gly Phe Val Met Ser Arg Ala Met Tyr Val
 530 535

<210> 24
 <211> 510
 <212> PRT
 <213> homo sapiens

<400> 24
 Met Pro Leu Ser Leu Gly Ala Glu Met Trp Gly Pro Glu Ala Trp Leu
 1 5 10 15

Leu Leu Leu Leu Leu Leu Ala Ser Phe Thr Gly Arg Cys Pro Ala Gly
 20 25 30

Glu Leu Glu Thr Ser Asp Val Val Thr Val Val Leu Gly Gln Asp Ala
 35 40 45

Lys Leu Pro Cys Phe Tyr Arg Gly Asp Ser Gly Glu Gln Val Gly Gln
 50 55 60

Val Ala Trp Ala Arg Val Asp Ala Gly Glu Gly Ala Gln Glu Leu Ala
 65 70 75 80

Leu Leu His Ser Lys Tyr Gly Leu His Val Ser Pro Ala Tyr Glu Gly
 85 90 95

Arg Val Glu Gln Pro Pro Pro Pro Arg Asn Pro Leu Asp Gly Ser Val
 100 105 110

Leu Leu Arg Asn Ala Val Gln Ala Asp Glu Gly Glu Tyr Glu Cys Arg
 115 120 125

Val Ser Thr Phe Pro Ala Gly Ser Phe Gln Ala Arg Leu Arg Leu Arg
 130 135 140

Val Met Val Pro Pro Leu Pro Ser Leu Asn Pro Gly Pro Ala Leu Glu
 145 150 155 160

Glu Gly Gln Gly Leu Thr Leu Ala Ala Ser Cys Thr Ala Glu Gly Ser
 165 170 175

Pro Ala Pro Ser Val Thr Trp Asp Thr Glu Val Lys Gly Thr Thr Ser
 180 185 190

Ser Arg Ser Phe Lys His Ser Arg Ser Ala Ala Val Thr Ser Glu Phe
 195 200 205

His Leu Val Pro Ser Arg Ser Met Asn Gly Gln Pro Leu Thr Cys Val
 210 215 220
 Val Ser His Pro Gly Leu Leu Gln Asp Gln Arg Ile Thr His Ile Leu
 225 230 235 240
 His Val Ser Phe Leu Ala Glu Ala Ser Val Arg Gly Leu Glu Asp Gln
 245 250 255
 Asn Leu Trp His Ile Gly Arg Glu Gly Ala Met Leu Lys Cys Leu Ser
 260 265 270
 Glu Gly Gln Pro Pro Pro Ser Tyr Asn Trp Thr Arg Leu Asp Gly Pro
 275 280 285
 Leu Pro Ser Gly Val Arg Val Asp Gly Asp Thr Leu Gly Phe Pro Pro
 290 295 300
 Leu Thr Thr Glu His Ser Gly Ile Tyr Val Cys His Val Ser Asn Glu
 305 310 315 320
 Phe Ser Ser Arg Asp Ser Gln Val Thr Val Asp Val Leu Asp Pro Gln
 325 330 335
 Glu Asp Ser Gly Lys Gln Val Asp Leu Val Ser Ala Ser Val Val Val
 340 345 350
 Val Gly Val Ile Ala Ala Leu Leu Phe Cys Leu Leu Val Val Val Val
 355 360 365
 Val Leu Met Ser Arg Tyr His Arg Arg Lys Ala Gln Gln Met Thr Gln
 370 375 380
 Lys Tyr Glu Glu Glu Leu Thr Leu Thr Arg Glu Asn Ser Ile Arg Arg
 385 390 395 400
 Leu His Ser His His Thr Asp Pro Arg Ser Gln Pro Glu Glu Ser Val
 405 410 415
 Gly Leu Arg Ala Glu Gly His Pro Asp Ser Leu Lys Asp Asn Ser Ser
 420 425 430
 Cys Ser Val Met Ser Glu Glu Pro Glu Gly Arg Ser Tyr Ser Thr Leu
 435 440 445
 Thr Thr Val Arg Glu Ile Glu Thr Gln Thr Glu Leu Leu Ser Pro Gly
 450 455 460
 Ser Gly Arg Ala Glu Glu Glu Glu Asp Gln Asp Glu Gly Ile Lys Gln
 465 470 475 480
 Ala Met Asn His Phe Val Gln Glu Asn Gly Thr Leu Arg Ala Lys Pro
 485 490 495
 Thr Gly Asn Gly Ile Tyr Ile Asn Gly Arg Gly His Leu Val
 500 505 510

<210> 25
 <211> 417
 <212> PRT
 <213> homo sapiens

<400> 25

Met	Ala	Arg	Ala	Met	Ala	Ala	Ala	Trp	Pro	Leu	Leu	Leu	Val	Ala	Leu
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Leu	Val	Leu	Ser	Trp	Pro	Pro	Pro	Gly	Thr	Gly	Asp	Val	Val	Val	Gln
			20					25					30		
Ala	Pro	Thr	Gln	Val	Pro	Gly	Phe	Leu	Gly	Asp	Ser	Val	Thr	Leu	Pro
		35					40					45			
Cys	Tyr	Leu	Gln	Val	Pro	Asn	Met	Glu	Val	Thr	His	Val	Ser	Gln	Leu
	50					55					60				
Thr	Trp	Ala	Arg	His	Gly	Glu	Ser	Gly	Ser	Met	Ala	Val	Phe	His	Gln
65					70					75					80
Thr	Gln	Gly	Pro	Ser	Tyr	Ser	Glu	Ser	Lys	Arg	Leu	Glu	Phe	Val	Ala
				85					90					95	
Ala	Arg	Leu	Gly	Ala	Glu	Leu	Arg	Asn	Ala	Ser	Leu	Arg	Met	Phe	Gly
			100					105					110		
Leu	Arg	Val	Glu	Asp	Glu	Gly	Asn	Tyr	Thr	Cys	Leu	Phe	Val	Thr	Phe
		115					120					125			
Pro	Gln	Gly	Ser	Arg	Ser	Val	Asp	Ile	Trp	Leu	Arg	Val	Leu	Ala	Lys
	130					135						140			
Pro	Gln	Asn	Thr	Ala	Glu	Val	Gln	Lys	Val	Gln	Leu	Thr	Gly	Glu	Pro
145					150					155					160
Val	Pro	Met	Ala	Arg	Cys	Val	Ser	Thr	Gly	Gly	Arg	Pro	Pro	Ala	Gln
				165					170					175	
Ile	Thr	Trp	His	Ser	Asp	Leu	Gly	Gly	Met	Pro	Asn	Thr	Ser	Gln	Val
			180					185						190	
Pro	Gly	Phe	Leu	Ser	Gly	Thr	Val	Thr	Val	Thr	Ser	Leu	Trp	Ile	Leu
		195					200					205			
Val	Pro	Ser	Ser	Gln	Val	Asp	Gly	Lys	Asn	Val	Thr	Cys	Lys	Val	Glu
	210					215					220				
His	Glu	Ser	Phe	Glu	Lys	Pro	Gln	Leu	Leu	Thr	Val	Asn	Leu	Thr	Val
225					230					235					240
Tyr	Tyr	Pro	Pro	Glu	Val	Ser	Ile	Ser	Gly	Tyr	Asp	Asn	Asn	Trp	Tyr
				245					250					255	
Leu	Gly	Gln	Asn	Glu	Ala	Thr	Leu	Thr	Cys	Asp	Ala	Arg	Ser	Asn	Pro
			260					265					270		
Glu	Pro	Thr	Gly	Tyr	Asn	Trp	Ser	Thr	Thr	Met	Gly	Pro	Leu	Pro	Pro
		275					280					285			

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Phe Ala Val Ala Gln Gly Ala Gln Leu Leu Ile Arg Pro Val Asp Lys
290 295 300

Pro Ile Asn Thr Thr Leu Ile Cys Asn Val Thr Asn Ala Leu Gly Ala
305 310 315 320

Arg Gln Ala Glu Leu Thr Val Gln Val Lys Glu Gly Pro Pro Ser Glu
325 330 335

His Ser Gly Ile Ser Arg Asn Ala Ile Ile Phe Leu Val Leu Gly Ile
340 345 350

Leu Val Phe Leu Ile Leu Leu Gly Ile Gly Ile Tyr Phe Tyr Trp Ser
355 360 365

Lys Cys Ser Arg Glu Val Leu Trp His Cys His Leu Cys Pro Ser Ser
370 375 380

Thr Glu His Ala Ser Ala Ser Ala Asn Gly His Val Ser Tyr Ser Ala
385 390 395 400

Val Ser Arg Glu Asn Ser Ser Ser Gln Asp Pro Gln Thr Glu Gly Thr
405 410 415

Arg

<210> 26
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide Primer

<400> 26
atatgtcgac gcgggcatgg cccggacccc cggcccgtcc ccgctgtgtc ctgg

54

<210> 27
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide Primer

<400> 27
atatgcggcc gcctaaacat accactccct cc

32

<210> 28
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide Primer

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<400> 28
ccctcaactg ctgacatcga

20

<210> 29
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide Primer

<400> 29
tgatcgtggc aattgtgtca t

21

<210> 30
<211> 1314
<212> DNA
<213> homo sapiens

<220>
<221> CDS
<222> (1)..(1314)
<223>

<400> 30
atg gcg cgg acc ctg cgg ccg tcc ccg ctg tgt cct gga ggc ggc aaa 48
Met Ala Arg Thr Leu Arg Pro Ser Pro Leu Cys Pro Gly Gly Gly Lys
1 5 10 15

gca caa ctt tcc tcc gct tct ctc ctc gga gcc ggg ctc ctg ctg cag 96
Ala Gln Leu Ser Ser Ala Ser Leu Leu Gly Ala Gly Leu Leu Leu Gln
20 25 30

ccc ccg acg cca cct ccg ctg ctg ctg ctg ctc ttc ccg ctg ctg ctc 144
Pro Pro Thr Pro Pro Pro Leu Leu Leu Leu Leu Phe Pro Leu Leu Leu
35 40 45

ttc tcc agg ctc tgt ggt gcc tta gct gga cca att att gtg gag cca 192
Phe Ser Arg Leu Cys Gly Ala Leu Ala Gly Pro Ile Ile Val Glu Pro
50 55 60

cat gtc aca gca gta tgg gga aag aat gtt tca tta aag tgt tta att 240
His Val Thr Ala Val Trp Gly Lys Asn Val Ser Leu Lys Cys Leu Ile
65 70 75 80

gaa gta aat gaa acc ata aca cag att tca tgg gag aag ata cat ggc 288
Glu Val Asn Glu Thr Ile Thr Gln Ile Ser Trp Glu Lys Ile His Gly
85 90 95

aaa agt tca cag act gtt gca gtt cac cat ccc caa tat gga ttc tct 336
Lys Ser Ser Gln Thr Val Ala Val His His Pro Gln Tyr Gly Phe Ser
100 105 110

gtt caa gga gaa tat cag gga aga gtc ttg ttt aaa aat tac tca ctt 384
Val Gln Gly Glu Tyr Gln Gly Arg Val Leu Phe Lys Asn Tyr Ser Leu
115 120 125

0997263-100501

52

gct gga gcg gta att gga gct gtt ctt gcc ctt ttc atc att gct atc 1152
 Ala Gly Ala Val Ile Gly Ala Val Leu Ala Leu Phe Ile Ile Ala Ile
 370 375 380

ttt gtg act gtg ctg ctg act cct cga aaa aaa aga cca tcc tat ctt 1200
 Phe Val Thr Val Leu Leu Thr Pro Arg Lys Lys Arg Pro Ser Tyr Leu
 385 390 395 400

gac aaa gtg att gac ctt cca ccc aca cat aaa cca cct cct ctg tat 1248
 Asp Lys Val Ile Asp Leu Pro Pro Thr His Lys Pro Pro Pro Leu Tyr
 405 410 415

gaa gaa cga tcc cca cct ttg cct cag aaa gac cta ttt cag gta tgt 1296
 Glu Glu Arg Ser Pro Pro Leu Pro Gln Lys Asp Leu Phe Gln Val Cys
 420 425 430

gtt cat gag tac act taa 1314
 Val His Glu Tyr Thr
 435

<210> 31
 <211> 437
 <212> PRT
 <213> homo sapiens

<400> 31
 Met Ala Arg Thr Leu Arg Pro Ser Pro Leu Cys Pro Gly Gly Gly Lys
 1 5 10 15

Ala Gln Leu Ser Ser Ala Ser Leu Leu Gly Ala Gly Leu Leu Leu Gln
 20 25 30

Pro Pro Thr Pro Pro Pro Leu Leu Leu Leu Leu Phe Pro Leu Leu Leu
 35 40 45

Phe Ser Arg Leu Cys Gly Ala Leu Ala Gly Pro Ile Ile Val Glu Pro
 50 55 60

His Val Thr Ala Val Trp Gly Lys Asn Val Ser Leu Lys Cys Leu Ile
 65 70 75 80

Glu Val Asn Glu Thr Ile Thr Gln Ile Ser Trp Glu Lys Ile His Gly
 85 90 95

Lys Ser Ser Gln Thr Val Ala Val His His Pro Gln Tyr Gly Phe Ser
 100 105 110

Val Gln Gly Glu Tyr Gln Gly Arg Val Leu Phe Lys Asn Tyr Ser Leu
 115 120 125

Asn Asp Ala Thr Ile Thr Leu His Asn Ile Gly Phe Ser Asp Ser Gly
 130 135 140

Lys Tyr Ile Cys Lys Ala Val Thr Phe Pro Leu Gly Asn Ala Gln Ser
 145 150 155 160

Ser Thr Thr Val Thr Val Leu Val Glu Pro Thr Val Ser Leu Ile Lys
 165 170 175

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Gly Pro Asp Ser Leu Ile Asp Gly Gly Asn Glu Thr Val Ala Ala Ile
 180 185 190
 Cys Ile Ala Ala Thr Gly Lys Pro Val Ala His Ile Asp Trp Glu Gly
 195 200 205
 Asp Leu Gly Glu Met Glu Ser Thr Thr Thr Ser Phe Pro Asn Glu Thr
 210 215 220
 Ala Thr Ile Ile Ser Gln Tyr Lys Leu Phe Pro Thr Arg Phe Ala Arg
 225 230 235 240
 Gly Arg Arg Ile Thr Cys Val Val Lys His Pro Ala Leu Glu Lys Asp
 245 250 255
 Ile Arg Tyr Ser Phe Ile Leu Asp Ile Gln Tyr Ala Pro Glu Val Ser
 260 265 270
 Val Thr Gly Tyr Asp Gly Asn Trp Phe Val Gly Arg Lys Gly Val Asn
 275 280 285
 Leu Lys Cys Asn Ala Asp Ala Asn Pro Pro Pro Phe Lys Ser Val Trp
 290 295 300
 Ser Arg Leu Asp Gly Gln Trp Pro Asp Gly Leu Leu Ala Ser Asp Asn
 305 310 315 320
 Thr Leu His Phe Val His Pro Leu Thr Phe Asn Tyr Ser Gly Val Tyr
 325 330 335
 Ile Cys Lys Val Thr Asn Ser Leu Gly Gln Arg Ser Asp Gln Lys Val
 340 345 350
 Ile Tyr Ile Ser Asp Val Pro Phe Lys Gln Thr Ser Ser Ile Ala Val
 355 360 365
 Ala Gly Ala Val Ile Gly Ala Val Leu Ala Leu Phe Ile Ile Ala Ile
 370 375 380
 Phe Val Thr Val Leu Leu Thr Pro Arg Lys Lys Arg Pro Ser Tyr Leu
 385 390 395 400
 Asp Lys Val Ile Asp Leu Pro Pro Thr His Lys Pro Pro Pro Leu Tyr
 405 410 415
 Glu Glu Arg Ser Pro Pro Leu Pro Gln Lys Asp Leu Phe Gln Val Cys
 420 425 430
 Val His Glu Tyr Thr
 435

<210> 32
 <211> 1533
 <212> DNA
 <213> homo sapiens

<400> 32
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 ctgctggcat catttacagg ccggtgcccc gcgggtgagc tggagacctc agacgtggta 120

actgtggtgc tggggccagga cgcaaaaactg ccctgcttct accgagggga ctccggcgag 180
 caagtggggc aagtggcatg ggctcgggtg gacgcgggcg aaggcgccca ggaactagcg 240
 ctactgcact ccaaatacgg gcttcatgtg agcccggctt acgagggccg cgtggagcag 300
 ccgcccggcc cagcgaaccc cctggacggc tcagtgtctc tgcgcaacgc agtgcaggcg 360
 gatgagggcg agtacgagtg ccgggtcagc accttccccg ccggcagctt ccaggcgcg 420
 ctgcggctcc gagtgatggt gcctccccctg ccctcactga atcctggtcc agcactagaa 480
 gagggccagg gcctgaccct ggcagcctcc tgcacagctg agggcagccc agcccccagc 540
 gtgacctggg acacggaggt caaaggcaca acgtccagcc gttccttcaa gcactcccg 600
 tctgctgccg tcacctcaga gttccacttg gtgcctagcc gcagcatgaa tgggcagcca 660
 ctgacttggt tgggtgtcca tcctggcctg ctccaggacc aaaggatcac ccacatcctc 720
 cacgtgtcct tccttgctga ggctctgtg aggggccttg aagacaaaaa tctgtggcac 780
 attggcagag aaggagctat gctcaagtgc ctgagtgaag ggcagcccc tccctcatac 840
 aactggacac ggctggatgg gcctctgccc agtggggtag gagtggatgg ggacactttg 900
 ggctttcccc cactgaccac tgagcacagc ggcactctac tctgccatgt cagcaatgag 960
 ttctcctcaa gggatttctc ggtcactgtg gatgttcttg acccccagga agactctggg 1020
 aagcaggtgg acctagtgtc agcctcgggt gtggtggtgg gtgtgatcgc cgcactcttg 1080
 ttctgccttc tgggtggtgg ggtggtgctc atgtcccgat accatcggcg caaggcccag 1140
 cagatgaccc agaaatatga ggaggagctg accctgacca gggagaactc catccggagg 1200
 ctgcattccc atcacacgga cccaggagc cagccggagg agagtgtagg gctgagagcc 1260
 gagggccacc ctgatagtct caaggacaac agtagctgct ctgtgatgag tgaagagccc 1320
 gagggccgca gttactccac gctgaccacg gtgagggaga tagaaacaca gactgaactg 1380
 ctgtctccag gctctgggcg ggccgaggag gaggaagatc aggatgaagg catcaaacag 1440
 gccatgaacc attttgttca ggagaatggg accctacggg ccaagcccac gggcaatggc 1500
 atctacatca atgggcgggg acacctggtc tga 1533

<210> 33
 <211> 1660
 <212> DNA
 <213> homo sapiens

<220>
 <221> CDS
 <222> (61)..(1596)
 <223>

<400> 33
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atg ccc ctg tcc ctg gga gcc gag atg tgg ggg cct gag gcc tgg ctg 108
 Met Pro Leu Ser Leu Gly Ala Glu Met Trp Gly Pro Glu Ala Trp Leu
 1 5 10 15

ctg ccg ctg cta ctg ctg gca tca ttt aca ggc cgg tgc ccc gcg ggt 156
 Leu Pro Leu Leu Leu Leu Ala Ser Phe Thr Gly Arg Cys Pro Ala Gly
 20 25 30

gag ctg gag acc tca gac gtg gta act gtg gtg ctg ggc cag gac gca 204
 Glu Leu Glu Thr Ser Asp Val Val Thr Val Val Leu Gly Gln Asp Ala
 35 40 45

aaa ctg ccc tgc ttc tac cga ggg gac tcc ggc gag caa gtg ggg caa 252
 Lys Leu Pro Cys Phe Tyr Arg Gly Asp Ser Gly Glu Gln Val Gly Gln
 50 55 60

gtg gca tgg gct cgg gtg gac gcg ggc gaa ggc gcc cag gaa cta gcg 300
 Val Ala Trp Ala Arg Val Asp Ala Gly Glu Gly Ala Gln Glu Leu Ala
 65 70 75 80

cta ctg cac tcc aaa tac ggg ctt cat gtg agc ccg gct tac gag ggc 348
 Leu Leu His Ser Lys Tyr Gly Leu His Val Ser Pro Ala Tyr Glu Gly
 85 90 95

cgc gtg gag cag ccg ccg ccc cca cgc aac ccc ctg gac ggc tca gtg 396
 Arg Val Glu Gln Pro Pro Pro Pro Arg Asn Pro Leu Asp Gly Ser Val
 100 105 110

ctc ctg cgc aac gca gtg cag gcg gat gag ggc gag tac gag tgc cgg 444
 Leu Leu Arg Asn Ala Val Gln Ala Asp Glu Gly Glu Tyr Glu Cys Arg
 115 120 125

gtc agc acc ttc ccc gcc ggc agc ttc cag gcg cgg ctg cgg ctc cga 492
 Val Ser Thr Phe Pro Ala Gly Ser Phe Gln Ala Arg Leu Arg Leu Arg
 130 135 140

gtg ctg gtg cct ccc ctg ccc tcg ctg aat cct ggt cca gca cta gaa 540
 Val Leu Val Pro Pro Leu Pro Ser Leu Asn Pro Gly Pro Ala Leu Glu
 145 150 155 160

gag ggc cag ggc ctg acc ctg gca gcc tcc tgc aca gct gag ggc agc 588
 Glu Gly Gln Gly Leu Thr Leu Ala Ala Ser Cys Thr Ala Glu Gly Ser
 165 170 175

cca gcc ccc agc gtg acc tgg gac acg gag gtc aaa ggc aca acg tcc 636
 Pro Ala Pro Ser Val Thr Trp Asp Thr Glu Val Lys Gly Thr Thr Ser
 180 185 190

agc cgt tcc ttc aag cac tcc cgc tct gct gcc gtc acc tca gag ttc 684
 Ser Arg Ser Phe Lys His Ser Arg Ser Ala Ala Val Thr Ser Glu Phe
 195 200 205

cac ttg gtg cct agc cgc agc atg aat ggg cag cca ctg act tgt gtg 732
 His Leu Val Pro Ser Arg Ser Met Asn Gly Gln Pro Leu Thr Cys Val
 210 215 220

gtg tcc cat cct ggc ctg ctc cag gac caa agg atc acc cac atc ctc 780
 Val Ser His Pro Gly Leu Leu Gln Asp Gln Arg Ile Thr His Ile Leu
 225 230 235 240

cac gtg tcc ttc ctt gct gag gcc tct gtg agg ggc ctt gaa gac caa 828
 His Val Ser Phe Leu Ala Glu Ala Ser Val Arg Gly Leu Glu Asp Gln
 245 250 255

aat ctg tgg cac att ggc aga gaa gga gct atg ctc aag tgc ctg agt 876
 Asn Leu Trp His Ile Gly Arg Glu Gly Ala Met Leu Lys Cys Leu Ser
 260 265 270

gaa ggg cag ccc cct ccc tca tac aac tgg aca cgg ctg gat ggg cct 924
 Glu Gly Gln Pro Pro Pro Ser Tyr Asn Trp Thr Arg Leu Asp Gly Pro
 275 280 285

ctg ccc agt ggg gta cga gtg gat ggg gac act ttg ggc ttt ccc cca 972
 Leu Pro Ser Gly Val Arg Val Asp Gly Asp Thr Leu Gly Phe Pro Pro
 290 295 300

ctg acc act gag cac agc ggc atc tac gtc tgc cat gtc agc aat gag 1020
 Leu Thr Thr Glu His Ser Gly Ile Tyr Val Cys His Val Ser Asn Glu
 305 310 315 320

T0500T" 89224660

ttc tcc tca agg gat tct cag gtc act gtg gat gtt ctt gca gac ccc 1068
 Phe Ser Ser Arg Asp Ser Gln Val Thr Val Asp Val Leu Ala Asp Pro
 325 330 335

cag gaa gac tct ggg aag cag gtg gac cta gtg tca gcc tcg gtg gtg 1116
 Gln Glu Asp Ser Gly Lys Gln Val Asp Leu Val Ser Ala Ser Val Val
 340 345 350

gtg gtg ggt gtg atc gcc gca ctc ttg ttc tgc ctt ctg gtg gtg gtg 1164
 Val Val Gly Val Ile Ala Ala Leu Leu Phe Cys Leu Leu Val Val Val
 355 360 365

gtg gtg ctc atg tcc cga tac cat cgg cgc aag gcc cag cag atg acc 1212
 Val Val Leu Met Ser Arg Tyr His Arg Arg Lys Ala Gln Gln Met Thr
 370 375 380

cag aaa tat gag gag gag ctg acc ctg acc agg gag aac tcc atc cgg 1260
 Gln Lys Tyr Glu Glu Glu Leu Thr Leu Thr Arg Glu Asn Ser Ile Arg
 385 390 395 400

agg ctg cat tcc cat cac acg gac ccc agg agc cag ccg gag gag agt 1308
 Arg Leu His Ser His His Thr Asp Pro Arg Ser Gln Pro Glu Glu Ser
 405 410 415

gta ggg ctg aga gcc gag ggc cac cct gat agt ctc aag gac aac agt 1356
 Val Gly Leu Arg Ala Glu Gly His Pro Asp Ser Leu Lys Asp Asn Ser
 420 425 430

agc tgc tct gtg atg agt gaa gag ccc gag ggc cgc agt tac tcc acg 1404
 Ser Cys Ser Val Met Ser Glu Glu Pro Glu Gly Arg Ser Tyr Ser Thr
 435 440 445

ctg acc acg gtg agg gag ata gaa aca cag act gaa ctg ctg tct cca 1452
 Leu Thr Thr Val Arg Glu Ile Glu Thr Gln Thr Glu Leu Leu Ser Pro
 450 455 460

ggc tct ggg cgg gcc gag gag gag gaa gat cag gat gaa ggc atc aaa 1500
 Gly Ser Gly Arg Ala Glu Glu Glu Glu Asp Gln Asp Glu Gly Ile Lys
 465 470 475 480

cag gcc atg aac cat ttt gtt cag gag aat ggg acc cta cgg gcc aag 1548
 Gln Ala Met Asn His Phe Val Gln Glu Asn Gly Thr Leu Arg Ala Lys
 485 490 495

ccc acg ggc aat ggc atc tac atc aat ggg cgg gga cac ctg gtc tga 1596
 Pro Thr Gly Asn Gly Ile Tyr Ile Asn Gly Arg Gly His Leu Val
 500 505 510

ccgcggccgc atataatcac tagtgaattc gcggccgcct gcaggtcgac catatgggag 1656
 agct 1660

<210> 34
 <211> 511
 <212> PRT
 <213> homo sapiens

<400> 34

Met Pro Leu Ser Leu Gly Ala Glu Met Trp Gly Pro Glu Ala Trp Leu
1 5 10 15

Leu Pro Leu Leu Leu Leu Ala Ser Phe Thr Gly Arg Cys Pro Ala Gly
20 25 30

Glu Leu Glu Thr Ser Asp Val Val Thr Val Val Leu Gly Gln Asp Ala
35 40 45

Lys Leu Pro Cys Phe Tyr Arg Gly Asp Ser Gly Glu Gln Val Gly Gln
50 55 60

Val Ala Trp Ala Arg Val Asp Ala Gly Glu Gly Ala Gln Glu Leu Ala
65 70 75 80

Leu Leu His Ser Lys Tyr Gly Leu His Val Ser Pro Ala Tyr Glu Gly
85 90 95

Arg Val Glu Gln Pro Pro Pro Pro Arg Asn Pro Leu Asp Gly Ser Val
100 105 110

Leu Leu Arg Asn Ala Val Gln Ala Asp Glu Gly Glu Tyr Glu Cys Arg
115 120 125

Val Ser Thr Phe Pro Ala Gly Ser Phe Gln Ala Arg Leu Arg Leu Arg
130 135 140

Val Leu Val Pro Pro Leu Pro Ser Leu Asn Pro Gly Pro Ala Leu Glu
145 150 155 160

Glu Gly Gln Gly Leu Thr Leu Ala Ala Ser Cys Thr Ala Glu Gly Ser
165 170 175

Pro Ala Pro Ser Val Thr Trp Asp Thr Glu Val Lys Gly Thr Thr Ser
180 185 190

Ser Arg Ser Phe Lys His Ser Arg Ser Ala Ala Val Thr Ser Glu Phe
195 200 205

His Leu Val Pro Ser Arg Ser Met Asn Gly Gln Pro Leu Thr Cys Val
210 215 220

Val Ser His Pro Gly Leu Leu Gln Asp Gln Arg Ile Thr His Ile Leu
225 230 235 240

His Val Ser Phe Leu Ala Glu Ala Ser Val Arg Gly Leu Glu Asp Gln
245 250 255

Asn Leu Trp His Ile Gly Arg Glu Gly Ala Met Leu Lys Cys Leu Ser
260 265 270

Glu Gly Gln Pro Pro Pro Ser Tyr Asn Trp Thr Arg Leu Asp Gly Pro
275 280 285

Leu Pro Ser Gly Val Arg Val Asp Gly Asp Thr Leu Gly Phe Pro Pro
290 295 300

Leu Thr Thr Glu His Ser Gly Ile Tyr Val Cys His Val Ser Asn Glu
305 310 315 320

092233-10301

Phe Ser Ser Arg Asp Ser Gln Val Thr Val Asp Val Leu Ala Asp Pro
 325 330 335
 Gln Glu Asp Ser Gly Lys Gln Val Asp Leu Val Ser Ala Ser Val Val
 340 345 350
 Val Val Gly Val Ile Ala Ala Leu Leu Phe Cys Leu Leu Val Val Val
 355 360 365
 Val Val Leu Met Ser Arg Tyr His Arg Arg Lys Ala Gln Gln Met Thr
 370 375 380
 Gln Lys Tyr Glu Glu Glu Leu Thr Leu Thr Arg Glu Asn Ser Ile Arg
 385 390 395 400
 Arg Leu His Ser His His Thr Asp Pro Arg Ser Gln Pro Glu Glu Ser
 405 410 415
 Val Gly Leu Arg Ala Glu Gly His Pro Asp Ser Leu Lys Asp Asn Ser
 420 425 430
 Ser Cys Ser Val Met Ser Glu Glu Pro Glu Gly Arg Ser Tyr Ser Thr
 435 440 445
 Leu Thr Thr Val Arg Glu Ile Glu Thr Gln Thr Glu Leu Leu Ser Pro
 450 455 460
 Gly Ser Gly Arg Ala Glu Glu Glu Asp Gln Asp Glu Gly Ile Lys
 465 470 475 480
 Gln Ala Met Asn His Phe Val Gln Glu Asn Gly Thr Leu Arg Ala Lys
 485 490 495
 Pro Thr Gly Asn Gly Ile Tyr Ile Asn Gly Arg Gly His Leu Val
 500 505 510

<210> 35
 <211> 1838
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Fusion Construct

<220>
 <221> CDS
 <222> (58)..(1800)
 <223>

<400> 35
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 atg ccc ctg tcc ctg gga gcc gag atg tgg ggg cct gag gcc tgg ctg 105
 Met Pro Leu Ser Leu Gly Ala Glu Met Trp Gly Pro Glu Ala Trp Leu
 1 5 10 15
 ctg ccg ctg cta ctg ctg gca tca ttt aca ggc cgg tgc ccc gcg ggt 153
 Leu Pro Leu Leu Leu Leu Ala Ser Phe Thr Gly Arg Cys Pro Ala Gly
 20 25 30

gag ctg gag acc tca gac gtg gta act gtg gtg ctg ggc cag gac gca	201
Glu Leu Glu Thr Ser Asp Val Val Thr Val Val Leu Gly Gln Asp Ala	
35 40 45	
aaa ctg ccc tgc ttc tac cga ggg gac tcc ggc gag caa gtg ggg caa	249
Lys Leu Pro Cys Phe Tyr Arg Gly Asp Ser Gly Glu Gln Val Gly Gln	
50 55 60	
gtg gca tgg gct cgg gtg gac gcg ggc gaa ggc gcc cag gaa cta gcg	297
Val Ala Trp Ala Arg Val Asp Ala Gly Glu Gly Ala Gln Glu Leu Ala	
65 70 75 80	
cta ctg cac tcc aaa tac ggg ctt cat gtg agc ccg gct tac gag ggc	345
Leu Leu His Ser Lys Tyr Gly Leu His Val Ser Pro Ala Tyr Glu Gly	
85 90 95	
cgc gtg gag cag ccg ccg ccc cca cgc aac ccc ctg gac ggc tca gtg	393
Arg Val Glu Gln Pro Pro Pro Pro Arg Asn Pro Leu Asp Gly Ser Val	
100 105 110	
ctc ctg cgc aac gca gtg cag gcg gat gag ggc gag tac gag tgc cgg	441
Leu Leu Arg Asn Ala Val Gln Ala Asp Glu Gly Glu Tyr Glu Cys Arg	
115 120 125	
gtc agc acc ttc ccc gcc ggc agc ttc cag gcg cgg cta cgg ctc cga	489
Val Ser Thr Phe Pro Ala Gly Ser Phe Gln Ala Arg Leu Arg Leu Arg	
130 135 140	
gtg ctg gtg cct ccc ctg ccc tcg ctg aat cct ggt cca gca cta gaa	537
Val Leu Val Pro Pro Leu Pro Ser Leu Asn Pro Gly Pro Ala Leu Glu	
145 150 155 160	
gag ggc cag ggc ctg acc ctg gca gcc tcc tgc aca gct gag ggc agc	585
Glu Gly Gln Gly Leu Thr Leu Ala Ala Ser Cys Thr Ala Glu Gly Ser	
165 170 175	
cca gcc ccc agc gtg acc tgg gac acg gag gtc aaa ggc aca acg tcc	633
Pro Ala Pro Ser Val Thr Trp Asp Thr Glu Val Lys Gly Thr Thr Ser	
180 185 190	
agc cgt tcc ttc aag cac tcc cgc tct gct gcc gtc acc tca gag ttc	681
Ser Arg Ser Phe Lys His Ser Arg Ser Ala Ala Val Thr Ser Glu Phe	
195 200 205	
cac ttg gtg cct agc cgc agc atg aat ggg cag cca ctg act tgt gtg	729
His Leu Val Pro Ser Arg Ser Met Asn Gly Gln Pro Leu Thr Cys Val	
210 215 220	
gtg tcc cat cct ggc ctg ctc cag gac caa agg atc acc cac atc ctc	777
Val Ser His Pro Gly Leu Leu Gln Asp Gln Arg Ile Thr His Ile Leu	
225 230 235 240	
cac gtg tcc ttc ctt gct gag gcc tct gtg agg ggc ctt gaa gac caa	825
His Val Ser Phe Leu Ala Glu Ala Ser Val Arg Gly Leu Glu Asp Gln	
245 250 255	
aat ctg tgg cac att ggc aga gaa gga gct atg ctc aag tgc ctg agt	873
Asn Leu Trp His Ile Gly Arg Glu Gly Ala Met Leu Lys Cys Leu Ser	
260 265 270	

099222-100504

gaa ggg cag ccc cct ccc tca tac aac tgg aca cgg ctg gat ggg cct 921
 Glu Gly Gln Pro Pro Pro Ser Tyr Asn Trp Thr Arg Leu Asp Gly Pro
 275 280 285

ctg ccc agt ggg gta cga gtg gat ggg gac act ttg ggc ttt ccc cca 969
 Leu Pro Ser Gly Val Arg Val Asp Gly Asp Thr Leu Gly Phe Pro Pro
 290 295 300

ctg acc act gag cac agc ggc atc tac gtc tgc cat gtc agc aat gag 1017
 Leu Thr Thr Glu His Ser Gly Ile Tyr Val Cys His Val Ser Asn Glu
 305 310 315 320

ttc tcc tca agg gat tct cag gtc act gtg gat gtt ctt gca gac ccc 1065
 Phe Ser Ser Arg Asp Ser Gln Val Thr Val Asp Val Leu Ala Asp Pro
 325 330 335

cag gaa gac tct ggg aag cag gtg gac cta gtg tca gcc tcg aga tct 1113
 Gln Glu Asp Ser Gly Lys Gln Val Asp Leu Val Ser Ala Ser Arg Ser
 340 345 350

tgt gac aaa act cac aca tgc cca ccg tgc cca gca cct gaa gcc gag 1161
 Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Glu
 355 360 365

ggc gcg ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc 1209
 Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
 370 375 380

atg atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc 1257
 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
 385 390 395 400

cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag 1305
 His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
 405 410 415

gtg cat aat gcc aag aca aag ccg cgg gag gag cag tac aac agc acg 1353
 Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
 420 425 430

tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat 1401
 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 435 440 445

ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc 1449
 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
 450 455 460

atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag 1497
 Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 465 470 475 480

gtg tac acc ctg ccc cca tcc cgg gag gag atg acc aag aac cag gtc 1545
 Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
 485 490 495

agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg 1593
 Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 500 505 510

097238 10501

gag tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct 1641
 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 515 520 525

ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tat agc aag ctc acc 1689
 Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
 530 535 540

gtg gac aag agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg 1737
 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 545 550 555 560

atg cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg 1785
 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 565 570 575

tct ccg ggt aaa tga actagttcta gagcggccgc ggatctgttt aaactagt 1838
 Ser Pro Gly Lys
 580

<210> 36
 <211> 580
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Fusion Construct

<400> 36
 Met Pro Leu Ser Leu Gly Ala Glu Met Trp Gly Pro Glu Ala Trp Leu
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Leu Pro Leu Leu Leu Leu Ala Ser Phe Thr Gly Arg Cys Pro Ala Gly
 20 25 30

Glu Leu Glu Thr Ser Asp Val Val Thr Val Val Leu Gly Gln Asp Ala
 35 40 45

Lys Leu Pro Cys Phe Tyr Arg Gly Asp Ser Gly Glu Gln Val Gly Gln
 50 55 60

Val Ala Trp Ala Arg Val Asp Ala Gly Glu Gly Ala Gln Glu Leu Ala
 65 70 75 80

Leu Leu His Ser Lys Tyr Gly Leu His Val Ser Pro Ala Tyr Glu Gly
 85 90 95

Arg Val Glu Gln Pro Pro Pro Pro Arg Asn Pro Leu Asp Gly Ser Val
 100 105 110

Leu Leu Arg Asn Ala Val Gln Ala Asp Glu Gly Glu Tyr Glu Cys Arg
 115 120 125

Val Ser Thr Phe Pro Ala Gly Ser Phe Gln Ala Arg Leu Arg Leu Arg
 130 135 140

Val Leu Val Pro Pro Leu Pro Ser Leu Asn Pro Gly Pro Ala Leu Glu
 145 150 155 160

Glu Gly Gln Gly Leu Thr Leu Ala Ala Ser Cys Thr Ala Glu Gly Ser
 165 170 175
 Pro Ala Pro Ser Val Thr Trp Asp Thr Glu Val Lys Gly Thr Thr Ser
 180 185 190
 Ser Arg Ser Phe Lys His Ser Arg Ser Ala Ala Val Thr Ser Glu Phe
 195 200 205
 His Leu Val Pro Ser Arg Ser Met Asn Gly Gln Pro Leu Thr Cys Val
 210 215 220
 Val Ser His Pro Gly Leu Leu Gln Asp Gln Arg Ile Thr His Ile Leu
 225 230 235 240
 His Val Ser Phe Leu Ala Glu Ala Ser Val Arg Gly Leu Glu Asp Gln
 245 250 255
 Asn Leu Trp His Ile Gly Arg Glu Gly Ala Met Leu Lys Cys Leu Ser
 260 265 270
 Glu Gly Gln Pro Pro Pro Ser Tyr Asn Trp Thr Arg Leu Asp Gly Pro
 275 280 285
 Leu Pro Ser Gly Val Arg Val Asp Gly Asp Thr Leu Gly Phe Pro Pro
 290 295 300
 Leu Thr Thr Glu His Ser Gly Ile Tyr Val Cys His Val Ser Asn Glu
 305 310 315 320
 Phe Ser Ser Arg Asp Ser Gln Val Thr Val Asp Val Leu Ala Asp Pro
 325 330 335
 Gln Glu Asp Ser Gly Lys Gln Val Asp Leu Val Ser Ala Ser Arg Ser
 340 345 350
 Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Glu
 355 360 365
 Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
 370 375 380
 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
 385 390 395 400
 His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
 405 410 415
 Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
 420 425 430
 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 435 440 445
 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
 450 455 460
 Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 465 470 475 480

09072363-10501
 T0500T-39221560

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
485 490 495

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
500 505 510

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
515 520 525

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
530 535 540

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
545 550 555 560

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
565 570 575

Ser Pro Gly Lys
580

<210> 37
<211> 497
<212> PRT
<213> homo sapiens

<400> 37
Glu Leu Gln Lys Arg Trp Ala Val Cys Leu Ser Thr Met Pro Leu Ser
1 5 10 15

Leu Gly Ala Glu Met Trp Gly Pro Glu Ala Trp Leu Leu Leu Leu Leu
20 25 30

Leu Leu Ala Ser Phe Thr Gly Arg Cys Pro Ala Gly Glu Leu Glu Thr
35 40 45

Ser Asp Val Val Thr Val Val Leu Gly Gln Asp Ala Lys Leu Pro Cys
50 55 60

Phe Tyr Arg Gly Asp Ser Gly Glu Gln Val Gly Gln Val Ala Trp Ala
65 70 75 80

Arg Val Asp Ala Gly Glu Gly Ala Gln Glu Leu Ala Leu Leu His Ser
85 90 95

Lys Tyr Gly Leu His Val Ser Pro Ala Tyr Glu Gly Arg Val Glu Gln
100 105 110

Pro Pro Pro Pro Arg Asn Pro Leu Asp Gly Ser Val Leu Leu Arg Asn
115 120 125

Ala Val Gln Ala Asp Glu Gly Glu Tyr Glu Cys Arg Val Ser Thr Phe
130 135 140

Pro Ala Gly Ser Phe Gln Ala Arg Leu Arg Leu Arg Val Leu Val Pro
145 150 155 160

0992268-100504

Pro Leu Pro Ser Leu Asn Pro Gly Pro Ala Leu Glu Glu Gly Gln Gly
 165 170 175
 Leu Thr Leu Ala Ala Ser Cys Thr Ala Glu Gly Ser Pro Ala Pro Ser
 180 185 190
 Val Thr Trp Asp Thr Glu Val Lys Gly Thr Thr Ser Ser Arg Ser Phe
 195 200 205
 Lys His Ser Arg Ser Ala Ala Val Thr Ser Glu Phe His Leu Val Pro
 210 215 220
 Ser Arg Ser Met Asn Gly Gln Pro Leu Thr Cys Val Val Ser His Pro
 225 230 235 240
 Gly Leu Leu Gln Asp Gln Arg Ile Thr His Ile Leu His Val Ser Phe
 245 250 255
 Leu Ala Glu Ala Ser Val Arg Gly Leu Glu Asp Gln Asn Leu Trp His
 260 265 270
 Ile Gly Arg Glu Gly Ala Met Leu Lys Cys Leu Ser Glu Gly Gln Pro
 275 280 285
 Pro Pro Ser Tyr Asn Trp Thr Arg Leu Asp Gly Pro Leu Pro Ser Gly
 290 295 300
 Val Arg Val Asp Gly Asp Thr Leu Gly Phe Pro Pro Leu Thr Thr Glu
 305 310 315 320
 His Ser Gly Ile Tyr Val Cys His Val Ser Asn Glu Phe Ser Ser Arg
 325 330 335
 Asp Ser Gln Val Thr Val Asp Val Leu Asp Pro Gln Glu Asp Ser Gly
 340 345 350
 Lys Gln Val Asp Leu Val Ser Ala Ser Val Val Val Val Gly Val Ile
 355 360 365
 Ala Ala Leu Leu Phe Cys Leu Leu Val Val Val Val Val Leu Met Ser
 370 375 380
 Arg Tyr His Arg Arg Lys Ala Gln Gln Met Thr Gln Lys Tyr Glu Glu
 385 390 395 400
 Glu Leu Thr Leu Thr Arg Glu Asn Ser Ile Arg Arg Leu His Ser His
 405 410 415
 His Thr Asp Pro Arg Ser Gln Ser Glu Glu Pro Glu Gly Arg Ser Tyr
 420 425 430
 Ser Thr Leu Thr Thr Val Arg Glu Ile Glu Thr Gln Thr Glu Leu Leu
 435 440 445
 Ser Pro Gly Ser Gly Arg Ala Glu Glu Glu Glu Asp Gln Asp Glu Gly
 450 455 460
 Ile Lys Gln Ala Met Asn His Phe Val Gln Glu Asn Gly Thr Leu Arg
 465 470 475 480

Ala Lys Pro Thr Gly Asn Gly Ile Tyr Ile Asn Gly Arg Gly His Leu
 485 490 495

Val

<210> 38
 <211> 402
 <212> PRT
 <213> homo sapiens

<400> 38

Glu Leu Gln Lys Arg Trp Ala Val Cys Leu Ser Thr Met Pro Leu Ser
 1 5 10 15

Leu Gly Ala Glu Met Trp Gly Pro Glu Ala Trp Leu Leu Leu Leu Leu
 20 25 30

Leu Leu Ala Ser Phe Thr Val Pro Pro Leu Pro Ser Leu Asn Pro Gly
 35 40 45

Pro Ala Leu Glu Glu Gly Gln Gly Leu Thr Leu Ala Ala Ser Cys Thr
 50 55 60

Ala Glu Gly Ser Pro Ala Pro Ser Val Thr Trp Asp Thr Glu Val Lys
 65 70 75 80

Gly Thr Thr Ser Ser Arg Ser Phe Lys His Ser Arg Ser Ala Ala Val
 85 90 95

Thr Ser Glu Phe His Leu Val Pro Ser Arg Ser Met Asn Gly Gln Pro
 100 105 110

Leu Thr Cys Val Val Ser His Pro Gly Leu Leu Gln Asp Gln Arg Ile
 115 120 125

Thr His Ile Leu His Val Ser Phe Leu Ala Glu Ala Ser Val Arg Gly
 130 135 140

Leu Glu Asp Gln Asn Leu Trp His Ile Gly Arg Glu Gly Ala Met Leu
 145 150 155 160

Lys Cys Leu Ser Glu Gly Gln Pro Pro Pro Ser Tyr Asn Trp Thr Arg
 165 170 175

Leu Asp Gly Pro Leu Pro Ser Gly Val Arg Val Asp Gly Asp Thr Leu
 180 185 190

Gly Phe Pro Pro Leu Thr Thr Glu His Ser Gly Ile Tyr Val Cys His
 195 200 205

Val Ser Asn Glu Phe Ser Ser Arg Asp Ser Gln Val Thr Val Asp Val
 210 215 220

Leu Asp Pro Gln Glu Asp Ser Gly Lys Gln Val Asp Leu Val Ser Ala
 225 230 235 240

Ser Val Val Val Val Gly Val Ile Ala Ala Leu Leu Phe Cys Leu Leu
245 250 255

Val Val Val Val Val Leu Met Ser Arg Tyr His Arg Arg Lys Ala Gln
260 265 270

Gln Met Thr Gln Lys Tyr Glu Glu Glu Leu Thr Leu Thr Arg Glu Asn
275 280 285

Ser Ile Arg Arg Leu His Ser His His Thr Asp Pro Arg Ser Gln Pro
290 295 300

Glu Glu Ser Val Gly Leu Arg Ala Glu Gly His Pro Asp Ser Leu Lys
305 310 315 320

Asp Asn Ser Ser Cys Ser Val Met Ser Glu Glu Pro Glu Gly Arg Ser
325 330 335

Tyr Ser Thr Leu Thr Thr Val Arg Glu Ile Glu Thr Gln Thr Glu Leu
340 345 350

Leu Ser Pro Gly Ser Gly Arg Ala Glu Glu Glu Glu Asp Gln Asp Glu
355 360 365

Gly Ile Lys Gln Ala Met Asn His Phe Val Gln Glu Asn Gly Thr Leu
370 375 380

Arg Ala Lys Pro Thr Gly Asn Gly Ile Tyr Ile Asn Gly Arg Gly His
385 390 395 400

Leu Val

<210> 39
<211> 498
<212> PRT
<213> homo sapiens

<400> 39

Glu Leu Gln Lys Arg Trp Ala Val Cys Leu Ser Thr Met Pro Leu Ser
1 5 10 15

Leu Gly Ala Glu Met Trp Gly Pro Glu Ala Trp Leu Leu Leu Leu Leu
20 25 30

Leu Leu Ala Ser Phe Ala Gly Arg Cys Pro Ala Gly Glu Leu Glu Thr
35 40 45

Ser Asp Val Val Thr Val Val Leu Gly Gln Asp Ala Lys Leu Pro Cys
50 55 60

Phe Tyr Arg Gly Asp Ser Gly Glu Gln Val Gly Gln Val Ala Trp Ala
65 70 75 80

Arg Val Asp Ala Gly Glu Gly Ala Gln Glu Leu Ala Leu Leu His Ser
85 90 95

Lys Tyr Gly Leu His Val Ser Pro Ala Tyr Glu Gly Arg Val Glu Gln
100 105 110

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Pro Pro Pro Pro Arg Asn Leu Leu Asp Gly Ser Val Leu Leu Arg Asn
115 120 125

Ala Val Gln Ala Asp Glu Gly Glu Tyr Glu Cys Arg Val Ser Thr Phe
130 135 140

Pro Ala Gly Ser Phe Gln Ala Arg Leu Arg Leu Arg Val Leu Val Pro
145 150 155 160

Pro Leu Pro Ser Leu Asn Pro Gly Pro Ala Leu Glu Glu Gly Gln Gly
165 170 175

Leu Thr Leu Ala Ala Ser Cys Thr Ala Glu Gly Ser Pro Ala Pro Ser
180 185 190

Val Thr Trp Asp Thr Glu Val Lys Gly Thr Thr Ser Ser Arg Ser Phe
195 200 205

Lys His Ser Arg Ser Ala Ala Val Thr Ser Glu Phe His Leu Val Pro
210 215 220

Ser Arg Ser Met Asn Gly Gln Pro Leu Thr Cys Val Val Ser His Pro
225 230 235 240

Gly Leu Leu Gln Asp Gln Arg Ile Thr His Ile Leu His Val Ser Phe
245 250 255

Leu Ala Glu Ala Ser Val Arg Gly Leu Glu Asp Gln Asn Leu Trp His
260 265 270

Ile Gly Arg Glu Gly Ala Met Leu Lys Cys Leu Ser Glu Gly Gln Pro
275 280 285

Pro Pro Ser Tyr Asn Trp Thr Arg Leu Asp Gly Pro Leu Pro Ser Gly
290 295 300

Val Arg Val Asp Gly Asp Thr Leu Gly Phe Pro Pro Leu Thr Thr Glu
305 310 315 320

His Ser Gly Ile Tyr Val Cys His Val Ser Asn Glu Phe Ser Ser Arg
325 330 335

Asp Ser Gln Val Thr Val Asp Val Leu Ala Asp Pro Gln Glu Asp Ser
340 345 350

Gly Lys Gln Val Asp Leu Val Ser Ala Ser Val Val Val Val Gly Val
355 360 365

Ile Ala Ala Leu Leu Phe Cys Leu Leu Val Val Val Val Val Leu Met
370 375 380

Ser Arg Tyr His Arg Arg Lys Ala Gln Gln Met Thr Gln Lys Tyr Glu
385 390 395 400

Glu Glu Leu Thr Leu Thr Arg Glu Asn Ser Ile Arg Arg Leu His Ser
405 410 415

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